

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 23, 2002, 05:15:37 ; Search time 1541.15 Seconds

(without alignments)
22372.323 Million cell updates/sec

Title: US-09-636-826-1
Perfect score: 2090
Sequence: 1 GATATCACACATTCGTCAT.....TCGGCTTTCGGCTGCTGCT 2090

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000.

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: GenEmbl:
1: gb_ba:*
2: gb_hng:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
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16: em_fun:*
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30: em_htgo_hum:*
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33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rnd:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2090	100.0	2090	6	AX088250
2	131	6.3	6644	6	E23356
3	131	6.3	7372	6	E23357
4	131	6.3	7797	6	E23355
5	131	6.3	7996	6	E23359
6	129.6	6.2	840	8	GMS0180K
7	129	6.2	213550	2	AC090493
8	128	6.1	160788	2	AL592166
9	127	6.1	160788	2	AL592166
10	126.4	6.0	14867	3	AE001398
11	123.2	5.9	217930	2	AC026471
12	122.6	5.9	99003	2	AL390756
13	121.6	5.8	1496	3	CEY53C12D
14	121.6	5.8	67970	3	PFMAL1P3
15	121.6	5.8	253305	3	PFMAL1P3
16	120.4	5.8	4601	3	DMU11584
17	120.4	5.8	19517	3	DMU37541
18	120.4	5.8	86827	3	PFMAL3P5
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20	120	5.7	169546	2	AC004157
21	119	5.7	201312	2	AC067900
22	118.6	5.7	183584	2	AC012492
23	118.6	5.7	303091	2	AC084799
24	118	5.6	159354	2	AL391425
25	118	5.6	326924	2	AC093082
26	117.4	5.6	172631	2	AC012566
27	117.2	5.6	137889	9	AC073269
28	117	5.6	50612	9	AL513350
29	116	5.6	44352	3	AE098501
30	116	5.6	143585	2	AC013349
31	115.2	5.5	124057	9	AP000770
32	114.6	5.5	126999	9	AL513328
33	114.2	5.5	54345	3	AC084152
34	114	5.5	114897	2	AP003624
35	114	5.5	298469	3	AE003846
36	113.2	5.4	1707	3	AF388909
37	113.2	5.4	1707	3	SDU49822
38	112.6	5.4	66441	3	PFMAL1P4
39	111.8	5.3	179902	2	AP003630
40	111.8	5.3	194212	2	AC092148
41	111.6	5.3	65691	2	PFMAL1P1
42	111.4	5.3	156550	2	AC015830
43	111.2	5.3	157957	9	AL445590
44	111	5.3	152878	3	CEY18D10A
45	110.8	5.3	153936	2	AC079863

ALIGNMENTS

RESULT 1
LOCUS AX088250 2090 bp DNA
DEFINITION Sequence 1 from Patent WO0114572.
ACCESSION AX088250
VERSION AX088250.1 GI:13397159
KEYWORDS
SOURCE
ORGANISM Beta vulgaris.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.

REFERENCE 1 (bases 1 to 2090)
AUTHORS Duwenti, E. and Rausch, T.
TITLE Plant gene expression, controlled by constitutive plant v-atpase promoters
JOURNAL BASF AKTIENGESellschaft (DE)
Patent: WO 0114572-A 1 01-MAR-2001;
location/Qualifiers

FEATURES
source 1..2090

/organism="Beta vulgaris"
 /db_xref="taxon:161934"
 /note="Promotor subunit c isoform 2"
 1..1923
 BASE COUNT 794 a 354 c 271 g 671 t
 ORIGIN

Query Match 100.0%; Score 2090; DB 6; Length 2090;
 Best Local Similarity 100.0%; Pred. No. 6.3e-258;
 Matches 2090; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATATCACACATTCGTCCATCGACATTTGCGACATTTAAATAGGTAAATCTTTT 60
 DB 1 GATATCACACATTCGTCCATCGACATTTGCGACATTTAAATAGGTAAATCTTTT 60
 QY 61 AACTTCAAGTATTTCCATTCATTCGACATTTATGATGTAAGTAAATGAGATATA 120
 DB 61 AACTTCAAGTATTTCCATTCATTCGACATTTATGATGTAAGTAAATGAGATATA 120
 QY 121 GGAATAGTGAAGAAGGCTTTATATTAATAGACTTAATTTGATTCATTTTCAATAT 180
 DB 121 GGAATAGTGAAGAAGGCTTTATATTAATAGACTTAATTTGATTCATTTTCAATAT 180
 QY 181 CTGAAAACAAGTATGATGAATTTGATTCATTTATGACACGTGATGAAGTAAAGA 240
 DB 181 CTGAAAACAAGTATGATGAATTTGATTCATTTATGACACGTGATGAAGTAAAGA 240
 QY 241 TTTAGTCTTTTAAATTTCCATATTAATTTTGGCCAAACTTTTGCATAATATC 300
 DB 241 TTTAGTCTTTTAAATTTCCATATTAATTTTGGCCAAACTTTTGCATAATATC 300
 QY 301 CATGTTGGAATTAATTTGAAAAACAACAATATCAAACTTTTGGCAACAATTT 360
 DB 301 CATGTTGGAATTAATTTGAAAAACAACAATATCAAACTTTTGGCAACAATTT 360
 QY 361 TACAAAATGCTATTCAGAAAAAAATTTACATTAAGTGAATGCAATTTGTAT 420
 DB 361 TACAAAATGCTATTCAGAAAAAAATTTACATTAAGTGAATGCAATTTGTAT 420
 QY 421 GAAAAATTTAAATTTCTTTCACTTAATTAATGAACTCAAGTGTAAATTTAGAAA 480
 DB 421 GAAAAATTTAAATTTCTTTCACTTAATTAATGAACTCAAGTGTAAATTTAGAAA 480
 QY 481 GGAGAAAAATTAATAATGACATTTTCATGGAATCAAAATGATGTAAGAAAA 540
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 QY 541 TTTATTTTAAATTAATTAATGAAATTTCAAGTGTAAATTTAGAAAAAGAAAAATTA 600
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 DB 721 GTAAACATCAATTTGTAATGAAATTTAGAAATTTAGAACAGAAAAAAATCTGAAT 780
 QY 781 GTCTTATCTTTGGTGTACAAATTTGGGATCAATGAAGAAATTTCTGAAATCCATCA 840
 DB 781 GTCTTATCTTTGGTGTACAAATTTGGGATCAATGAAGAAATTTCTGAAATCCATCA 840
 QY 841 AAACATTAATTAATTAAGAAAAATGATTAACCAAAAAAGAGACATGACATATTTTC 900
 DB 841 AAACATTAATTAATTAAGAAAAATGATTAACCAAAAAAGAGACATGACATATTTTC 900
 QY 901 GTAAAGAACATCATCTACTATTAATAAAGACATGCGCATATTTAGAAATGAAAA 960

DB 901 GTAAAGAACATCATCTACTATTAATAAAGACATGCGCATATTTAGAAATGAAAA 960
 QY 961 ACTATTCAAAATCACAATAATGATTAACAACATTAACAAGACATGAAGATCTTTTCA 1020
 DB 961 ACTATTCAAAATCACAATAATGATTAACAACATTAACAAGACATGAAGATCTTTTCA 1020
 QY 1021 CAAATGAGGTGACACTTAATTAATGACATTTGCAATTTTCAATTTTACTAGTAT 1080
 DB 1021 CAAATGAGGTGACACTTAATTAATGACATTTGCAATTTTCAATTTTACTAGTAT 1080
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 DB 1201 CCGGACACATTTTTCCTCATTTTATGATTTTACATTTGTTGTTGCAAAAGTGTAA 1260
 QY 1261 AACGTTTTCCCTTGGGTAAATTTACTCTTCCATGATGAAACCAATTTCTTTCAA 1320
 DB 1261 AACGTTTTCCCTTGGGTAAATTTACTCTTCCATGATGAAACCAATTTCTTTCAA 1320
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 DB 1321 AATGAGGAAAAACTGTTTCTCTATCTCTCTGTTACATTTCTGACATGACCTTAC 1380
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 DB 1381 TTTCCCTTTTATTTACTCTTCAATTTCTTCTGATGTAAGAACCAACAGGAAA 1440
 QY 1441 ACTAATTTTGAATTTGTTTCCATTTGTAATTTTTCATGAAATCTTTTAACCT 1500
 DB 1441 ACTAATTTTGAATTTGTTTCCATTTGTAATTTTTCATGAAATCTTTTAACCT 1500
 QY 1501 GAAATGTTTTACACCTTACCAACAGAGCCTGCTGTCATGATGACAGACGATTT 1560
 DB 1501 GAAATGTTTTACACCTTACCAACAGAGCCTGCTGTCATGATGACAGACGATTT 1560
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 QY 1801 CTCCCAATTTTCAATTTTAAATTAATCAGGGAAGTACACATTAATTAATCAAGGTA 1860
 DB 1801 CTCCCAATTTTCAATTTTAAATTAATCAGGGAAGTACACATTAATTAATCAAGGTA 1860
 QY 1861 AAAAATTAATAATAAAGAAAGATTAATTAACAAAAGAAATTTGCTCTGATATC 1920
 DB 1861 AAAAATTAATAATAAAGAAAGATTAATTAACAAAAGAAATTTGCTCTGATATC 1920
 QY 1921 CTCATATTTCAATCAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1980
 DB 1921 CTCATATTTCAATCAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1980
 QY 1981 TCGATCAAGCATTCATGAGACACCTTCCGATCATCACATCAAAAAAATGTCAAG 2040

Db 1981 TCGGATACAGCAATTTCATCGAACAACCTTCCGATCATACCACTCAAAAAATGTCAACG 2010

Qy 2041 TCTTTACGGCGATGAACGCGCCGTTCTCGGCTTTTCTGGGTGCTGCT 2090

Db 2041 TCTTTACGGCGATGAACGCGCCGTTCTCGGCTTTTCTGGGTGCTGCT 2090

RESULT	2						
E23356							
LOCUS	E23356	6644 bp	DNA		PAT	07-FEB-2001	
DEFINITION	Virus vector system expressing apoptosis-related gene.						
ACCESSION	E23356						
VERSION	E23356.1	GI:13024379					
KEYWORDS	JP 199075859-A/2.						
SOURCE	unidentified.						
ORIGIN	unidentified.						

REFERENCE 1 (bases 1 to 6644)
AUTHORS Hirofumi,H.
TITLE Virus vector system expressing apoptosis-related gene
JOURNAL Patent: JP 1999075859-A 2 23-MAR-1999;
D. D. TRANQUAN, et al.

COMMENT	OS
	Unidentified
PN	JP 1999075859-A/2
PD	23-MAR-1999
PF	08-SEP-1997 JP 1997259235

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PC C12N15/09,C12N5/10,C12N7/00//A61K35/76,A61K48/00,(C12N5/10, PC
C12R1:91) ,
PC (C12N7/00,C12R1:92),C12N15/00,C12N5/00,(C12N5/00,C12R1:91) CC
Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..6644
FT /organism='Unidentified'.

FEATURES
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BASE COUNT      2166 a 1573 c 1424 g 1481 t

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Matches 341;	Conservative 0;	Mismatches 350;	Indels 0;	Gaps 0;

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QY	382	AAAAAATTACATTACTTGCGAATCAATGTGTATGAAAAATTTAAATTTCTTT	441
Db	3801	AA	3860A
QY	442	CACCTATTAATTGAAACTCAAACTGTTTAAATTTAGAAAAAGGAAAAATAAAAATGACC	501
Db	3861	AA	3920A
QY	502	ATTTCATGCGAAATCAATGTGTATGAAAAACTTAAATTTTATTTAAATATAATGA	561
Db	3921	AA	3980A
QY	562	AATTCAAAGTGTAAATTTAGAAAAAGGAAAAATTTAAATGACCATTCATTCAAAT	621
Db	3981	AA	4040A
QY	622	CAGATGTGTATGAAAAATTTAAATTTTATTCAAATATAATGAACTCAAACTGTGA	681
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[illegible][illegible]

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 7372)
Hirotsumi, H.
Virus vector system expressing apoptosis-related gene
Patent: JP 1999075859-A 3 23-MAR-1999;
P. B. P. TENCROU KY

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

COMMENT	OS	Homo sapiens (human)
PN	JP 1999075859-A/3	
PD	23-MAR-1999	
PF	08-SEP-1997 JP 1997259235	

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PC      HIROFUMI HAMADA
PC      C12N15/09, C12N15/10, C12N7/00//A61K35/76, A61K48/00, (C12N5/10, PC
C12R1: 91) /
PC      (C12N7/00, C12R1: 92), C12N15/00, C12N5/00, (C12N5/00, C12R1: 91) CC
Strandedness: Double;
CC      Topology: Linear;
FH      Key      Location/Qualifiers
FT      source      1..7372
FT      Location/Qualifiers
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        /db_xref="taxon:9606"
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Matches 341; Conservative	0;	Mismatches 350;	Indels 0;	Gaps 0;
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Db 4469	AAA	4528		
OY 382	AAAAAAAAATTACATTTACTTGGCAATCAATTTGTATGAAAAATTTAAATTTTCCTT	441		
Db 4529	AAA	4588		

BASE COUNT	2542 a	1760 c	1656 g	1839 t	ORIGIN
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Matches 341	Conservative	0	Mismatches 350	Indels 0	Gaps 0
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Db	4894	AAA	4953		
Qy	382	AAAAAAATTACATCTACTTGGCAATCAATTTGTATGAAAAATTTAAATTCCTT	441		
Db	4954	AAA	5013		
Qy	442	CACCTTAATTTGAACCTCAAGTGTTAAATTTGACAAAAGAGAAAATTAATAATGACC	501		
Db	5014	AAA	5073		
Qy	502	ATTTCATGCGAATCAATTTGTGTGAAAAACCTTAAATTTTAAATTAATTTGA	561		
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Qy	562	AATTCAAAGTGTAAATTTAGAAAAAGAGAAAAATTAATAAGCAATTCATTCAAAT	621		
Db	5134	AAA	5193		
Qy	622	CAGATTGTATGAAAAATTTAAATTTTTCATTAATATTTGAACCTCAAGTGTGA	681		
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Db	5314	AAA	5373		
Qy	802	ATTTTGGATCATAAAGAAATTACGGAATTCATTCAAAACATATTAATTACAAA	861		
Db	5374	AAA	5433		
Qy	862	ATGATATAAACCACAAAAAGAGAACATGACGATATTTTCGTAAGAACATCATCTGATT	921		
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Qy	922	ATAAAGAACATGCGCATTTAGAAATTGAGAACAAAACTATTCATAATTCACAAAAT	981		
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LOCUS	E23359	7996 bp	DNA	PAT	07-FEB-2001
DEFINITION	Virus vector system expressing apoptosis-related gene.				
ACCESSION	E23359				
VERSION	E23359.1	GI:13024382			
KEYWORDS	JP_1999075859-A/5.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 7996)				
AUTHORS	Hirofumi, H.				
TITLE	Virus vector system expressing apoptosis-related gene				

JOURNAL Patent: JP 1999075859-A 5 23-MAR-1999;
R B R JENSEN KK
OS Homo sapiens (human)
PN JP 1999075859-A/5
PD 23-MAR-1999
PF 08-SEP-1997 JP 1997259235

PC HIRUFUMI HAWADA
PC C12N15/09, C12N5/10, C12N7/00//A61K35/76, A61K48/00, (C12N5/10, PC
C12R1:91),
PC (C12N7/00, C12R1:92), C12N15/00, C12N5/00, (C12N5/00, C12R1:91) CC
Strandedness: Double;
CC Topology: Linear;
FH Key
FT source
FT Location/Qualifiers
1.7996
/organism="Homo sapiens (human)"

BASE COUNT 2463 a 2015 c 1829 g 1689 t
ORIGIN

Query Match 6.3%, Score 131; DB 6; Length 7996;
Best Local Similarity 49.3%; Pred. No. 2.8e-08;
Matches 341; Conservative 0; Mismatches 350; Indels 0; Gaps 0;

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OY 382 AAAAAAATTTACATTAACCTGCAATCAATTTGTATGAAAAATTTAAATTTCCCTT 441
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 5153 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5212
OY 442 CACCATATATGAACTCAAGCTTTAAATTTGAAAAGAGAAAAATAAATATGACC 501
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 5213 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5272
OY 502 ATTTCATCGAATCAATTTGTATGAAAACTTTAAATTTTAAATATATATGA 561
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 5273 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5332
OY 562 AATTCAGTGTAAATTTGAAAAGAGAAAAATTTAAATGACCTTCATTCATAAT 621
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DB 5333 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5392
OY 622 CAGATTTGTATGAAAAATTTAAATTTTTCATTAATATATGAACTCAAGTGA 681
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 5393 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5452
OY 682 ACATTTAGAAAAGAGAAAAATTTAAATGATGAAAAATTTGTAAACATCAATTTGTGA 741
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DB 5453 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5512
OY 742 TCAGATTTTGAAGTTGACAGAAAAAACTGAAATTTCTTATCTTTTGGTTACA 801
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 5513 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5572
OY 802 ATTTGGATCATTAAGAAATTTACTGAATCCATTCAAAACATATTAATTCAGAAA 861
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DB 5573 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5632
OY 862 ATGATTAACCAAAAAAGAGAACATGAGATTTTCGTAAGAAGACATCATCTGATT 921
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DB 5633 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5692
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DB 5693 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5752
OY 982 GGATTAACACATACAAAAGACATGAAGAAT 1012

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DB 5753 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAAT 5783

RESULT 6
CNS0180K/c
LOCUS
DEFINITION
CNS0180K 840 bp mRNA PIN 02-SEP-1999
Botrytis cinerea strain T4 cDNA library under conditions of
nitrogen deprivation.
AL110675
VERSION
AL110675.1 GI:5824962
KEYWORDS
cDNA library; nitrogen deprivation.
SOURCE
Botryotinia fuckeliana
ORGANISM
Botryotinia fuckeliana
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Sclerotiniaceae; Botryotinia.

REFERENCE
1 (bases 1 to 840)
Bitton, F., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y.
TITLE
Direct Submission
JOURNAL
Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
78026 Versailles, France
2 (bases 1 to 840)
REFERENCE
Genoscope.
TITLE
Direct Submission
JOURNAL
Submitted (01-SEP-1999) Genoscope - Centre National de Séquençage :
CP 5706 91057 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT
The cDNA library to be analyzed within the framework of this
project was created using a Botrytis cinerea strain which was grown
under conditions of nitrogen deprivation, which is the normal
situation for B. cinerea during its development on its host plant.
The library was produced in an oriented direction, in the pBSII
vector.

FEATURES
source
1.840
/organism="Botryotinia fuckeliana"
/strain="T4"
/db_xref="taxon:40559"
/note="Genoscope sequence ID : W3B091"

BASE COUNT 151 a 23 c 79 g 539 t 48 others
ORIGIN

Query Match 6.2%; Score 129.6; DB 8; Length 840;
Best Local Similarity 47.4%; Pred. No. 5.7e-08;
Matches 334; Conservative 0; Mismatches 367; Indels 3; Gaps 1;

```

OY 405 AAATCAATTTGTATGAAAAATTTAAATTTCTTTCACCTATATGAACTCAAGT 464
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 835 ATTAATTAATTAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 776
OY 465 GTTAAATTTAGAAAAGAGAAAAATAAATGACCATTTTCATCGAATCAATTTGTG 524
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 775 TAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 716
OY 525 TATGAAAACCTTAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTTGA 584
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 715 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 656
OY 585 AAGAGAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 644
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 655 AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 596
OY 645 ATTTTATTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 704
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 595 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 536
OY 705 AAATGATGAATTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 764
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 535 AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 476
OY 765 GAAAAAATTAATTTGCTTATCTTTTGGTTGCAATTTGGGATTAAGAAATTA 824
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

COMMENT

*	1	100656:	contlg of 100656 bp in length
*	100657	102023:	gap of unknown length
*	102024	172443:	contlg of 70420 bp in length
*	172444	173810:	gap of unknown length
*	173811	210022:	contlg of 36212 bp in length

QY 872 CCAAAAAAAAAAGAACATGACCATATTTTCGTAAAGACATCATCTGATTATAAAGAAC 931
 Db 208734 TATAATANNAAAAAAAAAATATTAAATTAATANTAAAAANAAATTTAAATAATCTAANNCANNA 20867
 QY 932 ATCCGATATTGAAATTTGAAAGACAAAAACATTTCAAAATCAGCAAAATGGATTAACAC 991

FEATURES
SOURCE

Db 65165 AATTATATAATATTAATATATAAATAAGTATTTATGAATATA 65106

QY 518 AATTGTGTATGAAACTTAAATTTTATTTAAATATATGAAATTCAGACTGTAA 577
 Db 65105 TATGAT 65046
 QY 578 ATTGAGAAAGAGAGAAATTTAAATGACCATTCATTCAGAAATCGATGTGTAGAA- 636
 Db 65045 ATATATACAT 64986
 QY 637 AAATTTAATTTTATTTTCAATATATATGAACTCAAGTGTGACATTTAGAAAAGA 696
 Db 64985 AT 64926
 QY 697 GAAATTTAAATGATGAAATTTGTAACATTCATTCGTAAGTGTGAAATTCAGATTTAGAGT 756
 Db 64925 AAT 64866
 QY 757 TAGACAG 816
 Db 64865 TAT 64806
 QY 817 AGAATTTACTGAAATTCATATCAAACTATTTATATATTCAGAAATGAAATTAACCAA 876
 Db 64805 AAT 64746
 QY 877 AAAAG 936
 Db 64745 AAT 64686
 QY 937 CATATTTAGAAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 996
 Db 64685 GAT 64626
 QY 997 AAGA 1000
 Db 64625 AATA 64622

RESULT 9
 AL592166
 LOCUS 160788 bp DNA HTG 19-JUL-2001
 DEFINITION Homo sapiens chromosome 1 clone RP11-269F19, *** SEQUENCING IN
 AL592166
 ACCESSION AL592166.5 GI:14626208
 VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 160788)
 REFERENCE
 AUTHORS McLay, K.
 TITLE Direct Submission
 JOURNAL Submitted (18-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 requests: clonerequest@sanger.ac.uk
 On Jul 7, 2001 this sequence version replaced gi:14588772.
 COMMENT
 ----- Genome Center
 Center: Sanger Centre
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: humquery@sanger.ac.uk
 ----- Project Information
 Center project name: BA269F19
 ----- Summary Statistics
 Assembly program: XGAP4; version 4.5
 Sequencing vector: plasmid; L08752; 100% of reads
 Chemistry: Dye-terminator ET-amersham; 2% of reads
 Dye-terminator Big Dye; 97% of reads
 Consensus quality: 158006 bases at least Q40
 Consensus quality: 158812 bases at least Q30
 Consensus quality: 159376 bases at least Q20
 Insert size: 159988; sum-of-ctrls

Insert size: 172334; 4.2% error; agarose-tp
 Quality coverage: 9.97x in Q20 bases; sum-of-ctrls quality
 coverage: 9.32x in Q20 bases; agarose-tp

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 9 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 4065: contig of 4065 bp in length
 * 4066 4165: gap of 100 bp
 * 4166 17933: contig of 13768 bp in length
 * 17934 18033: gap of 100 bp
 * 18034 43303: contig of 25270 bp in length
 * 43304 43403: gap of 100 bp
 * 43404 64504: contig of 21101 bp in length
 * 64505 64604: gap of 100 bp
 * 64605 95691: contig of 31087 bp in length
 * 95692 95791: gap of 100 bp
 * 95792 118401: contig of 22610 bp in length
 * 118402 118501: gap of 100 bp
 * 118502 136017: contig of 17516 bp in length
 * 136018 136117: gap of 100 bp
 * 136118 145258: contig of 9414 bp in length
 * 145259 145358: gap of 100 bp
 * 145359 160788: contig of 15430 bp in length.

FEATURES

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 /clone_id="RPC1-11.1"
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 fragment_chain:1"
 misc_feature
 4166..17933
 /note="assembly_fragment:00316
 fragment_chain:1"
 misc_feature
 18034..43303
 /note="assembly_fragment:00012
 fragment_chain:1"
 misc_feature
 43404..64504
 /note="assembly_fragment:00094
 fragment_chain:1"
 misc_feature
 64605..95691
 /note="assembly_fragment:01356
 fragment_chain:2"
 misc_feature
 95792..118401
 /note="assembly_fragment:01103
 fragment_chain:2"
 misc_feature
 118502..136017
 /note="assembly_fragment:01760
 fragment_chain:3"
 misc_feature
 136118..145258
 /note="assembly_fragment:02686
 fragment_chain:3"
 misc_feature
 145359..160788
 /note="assembly_fragment:00411
 fragment_chain:3
 clone_end:17
 vector_side:right"
 BASE COUNT 40346 a 38964 c 40180 g 40496 t 802 others
 ORIGIN

Query Match 6.1%; Score 127; DB 2; Length 160788;
 Best Local Similarity 47.2%; Pred. No. 5.9e-08;
 Matches 451; Conservative 0; Mismatches 500; Indels 4; Gaps 2;

Query Match 6.0%; Score 126.4; DB 3; Length 14867;
 Best Local Similarity 48.5%; Pred. No. 9.8e-08;
 Matches 506; Conservative 0; Mismatches 521; Indels 17; Gaps 5;

```

QY 66 TCAAGTATTCACATTAGTCGACTATATGTAAGTAAAGATGAATATGCAAT 125
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 9656 TTAATATATTAATAATATATATATATATATATATATATATATATATAT 9597
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 126 TAGTTGAAGAAGGCTTTATATATATATATATATATATATATATATATAT 185
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 9596 TATATATATATATATATATATATATATATATATATATATATATATAT 9537
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 186 AACAGATATATATATATATATATATATATATATATATATATATATAT 244
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 9536 AAAAAATATATATATATATATATATATATATATATATATATATATAT 9477
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 245 GTTCCTTTTATATATATATATATATATATATATATATATATATATAT 304
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 9476 TATATATATATATATATATATATATATATATATATATATATATATAT 9417
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 305 TTGGAATATATATATATATATATATATATATATATATATATATATAT 364
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 9416 TATATATATATATATATATATATATATATATATATATATATATATAT 9357
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 365 AAAATCATTTCAGAAAAAATTTACATTAATCTGGCAATCA--TATGTGATGA 422
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 9356 TAAATATATATATATATATATATATATATATATATATATATATATAT 9297
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 423 AAAATTTAAATTTCTTCACCTATATATATATATATATATATATATATAT 473
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 9296 AAAATTTAAATTTATATATATATATATATATATATATATATATATATAT 9237
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 474 TAGAAAAAGAAAAATAAAAATGACCATTCATCGCAATCAATTTGTATGAAAA 533
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 9236 TATATATATATATATATATATATATATATATATATATATATATATAT 9177
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 534 CTAAATTTATATATATATATATATATATATATATATATATATATATAT 593
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 9176 AATATATATATATATATATATATATATATATATATATATATATATAT 9117
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 594 AAAATTAATGACCATTCATCAAAATCAGATTTGTATGAAAAATTTAAATTTTAT 653
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 9116 TAAATATATATATATATATATATATATATATATATATATATATATAT 9057
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 654 TCAATATATATGCAACTCAAGTGCAGACATTTAGAAAAAGGAAAAATTTAAATGATG 713
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 9056 TTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8997
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 714 AAAATTTGTAAACATCAATTTGGAATCAGATTTAGAACTTAGCAAGAAAAA 773
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8996 AATTAATTTATATATATATATATATATATATATATATATATATATAT 8937
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 774 CTGAATTTCTTATACCTTTGCGTTACATTTGGGATCTAAAGAAATTTACTGAATCC 833
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8936 AAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8877
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 834 ATATCAAAACATATATATATATATATATATATATATATATATATATAT 893
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8876 AAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8817
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 894 ATATTTGTAAAGACATCACTACTGATTT--ATAAAGACATCGCATATTAGAAATGAG 951
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8816 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 8757
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 952 AAACAAAAAATCTATTCAAAAATCAGAAAAATGATA---ACAACATCAAGAACATGAAA 1008
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8756 TAACTAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8697
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1009 GAATCTATTCACAAATGAGTGAGTGAATTAATTAATTAATTAATTAATTA 1068
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8696 AAAATTTATATATATATATATATATATATATATATATATATATATAT 8637
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1069 CTACTTATATATAGCCCTAAAAAT 1092
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

DB 8636 AAAATATATATATATATATATATATATATATATATATATATATATAT 8613
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
RESULT 11
AC026471
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
Project Information
Center Project Name: 0
Center clone name: RPC1-11_452L6
-----
Summary Statistics
Consensus quality: 153818 bases at least Q40
Consensus quality: 167559 bases at least Q30
Consensus quality: 175248 bases at least Q20
Estimated insert size: 191131; agarose-fp estimation
Estimated insert size: 214130; sum-of-contigs estimation
Quality coverage: 4.11 in Q20 bases; agarose-fp estimation
Quality coverage: 3.67 in Q20 bases; sum-of-contigs estimation
NOTE: This is a 'working draft' sequence. It currently
* consists of 39 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
1414 1413: contig of 1413 bp in length
1514 1513: gap of unknown length
2719 2718: contig of 1205 bp in length
2819 2818: gap of unknown length
3929 3928: contig of 1110 bp in length
4029 4028: gap of unknown length
5162 5161: contig of 1133 bp in length
5262 5261: gap of unknown length
6367 6366: contig of 1105 bp in length
6467 6466: gap of unknown length
7573 7573: contig of 1107 bp in length
7674 7673: gap of unknown length
9154 9154: contig of 1481 bp in length
9255 9254: gap of unknown length
10632 10631: contig of 1277 bp in length
10633 10632: gap of unknown length
11858 11858: contig of 1227 bp in length
11859 11859: gap of unknown length
13418 13418: contig of 1460 bp in length
13519 13518: gap of unknown length
14759 14758: contig of 1240 bp in length
14759 14758: gap of unknown length

```

QY 132 AAAAGGCTTATATATAATTAGACTAAATTTGATTCATTTTCATATATCTGAAAAACAG 191
||| | | | | | | | | | | | | | | | |
Db 25297 AAATNTTTTTTAATATATAATATAAANAATAAAAAAAAAATAAANAATAATAT 25366

RESULT	12
LOCUS	AL390756/C
DEFINITION	AL390756 99003 bp DNA
ACCESSION	Homo sapiens chromosome 1 clone RP11-378A4, *** SEQUENCING IN PROGRESS ***; 2931005
VERSION	AL390756
KEYWORDS	AL390756.2 GI:991005
SOURCE	HTG; HTGS_PHASE1; HTGS_CANCELLED.
ORGANISM	human.
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE	1 (bases 1 to 99003)
AUTHORS	McLay, K.
TITLE	Direct Submission

JOURNAL
Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Aug 27, 2000 this sequence version replaced gi:5581725.

Genome Center

Center: Sanger Centre

Center code: SC

Web site: <http://www.sanger.ac.uk>Contact: humquerry@sanger.ac.uk

Project Information

Center project name: BA378A4

Summary Statistics

Assembly program: XGAP4; version 4.5

Sequencing vector: plasmid; L08752; 100% of reads Chemistry:

Dye-terminator Big Dye; 73% of reads

Dye-terminator Big Dye; 73% of reads

Consensus quality: 84348 bases at least Q40

Consensus quality: 92139 bases at least Q30

Insert size: 96203; sum-of-contigs

Insert size: 188174; 2.5% error; agarose-fp

Quality coverage: 2.40x in Q20 bases; sum-of-contigs quality

coverage: 1.82x in Q20 bases; agarose-fp

NOTE: This is a 'working draft' sequence. It currently
* consists of 29 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1
2814 2913: contig of 2813 bp in length
2914 2913: gap of 100 bp
7381 7480: contig of 4467 bp in length
7481 11099: contig of 3619 bp in length
11100 11199: gap of 100 bp
11200 13897: contig of 2698 bp in length
13898 13997: gap of 100 bp
13998 16453: contig of 2456 bp in length
16454 16553: gap of 100 bp
16554 19055: contig of 2502 bp in length
19056 19155: gap of 100 bp
19156 21888: contig of 2733 bp in length
21889 21988: gap of 100 bp
21989 25542: contig of 3554 bp in length
25543 25642: gap of 100 bp
25643 30331: contig of 4689 bp in length
30332 30431: gap of 100 bp
30432 32487: contig of 2056 bp in length
32488 32587: gap of 100 bp
32588 36034: contig of 3447 bp in length
36035 36134: gap of 100 bp
36135 38214: contig of 2080 bp in length
38215 38314: gap of 100 bp
38315 40332: contig of 2018 bp in length
40333 40432: gap of 100 bp
40433 43002: contig of 2370 bp in length
43003 43102: gap of 100 bp
43103 48212: contig of 5110 bp in length
48213 48312: gap of 100 bp
48313 52476: contig of 4164 bp in length
52477 52576: gap of 100 bp
52577 54653: contig of 2077 bp in length
54654 54753: gap of 100 bp
54754 57605: contig of 2852 bp in length
57606 57705: gap of 100 bp
57706 60028: contig of 2323 bp in length
60029 60128: gap of 100 bp
60129 63554: contig of 3426 bp in length
63555 63654: gap of 100 bp
63655 66479: contig of 2825 bp in length

66480 66579: gap of 100 bp
66580 72814: contig of 6235 bp in length
72815 72914: gap of 100 bp
72915 78995: contig of 6081 bp in length
78996 79095: gap of 100 bp
79096 82552: contig of 3457 bp in length
82553 82652: gap of 100 bp
82653 85473: contig of 2821 bp in length
85474 85573: gap of 100 bp
85574 88078: contig of 2505 bp in length
88079 88178: gap of 100 bp
88179 90954: contig of 2776 bp in length
90955 91054: gap of 100 bp
91055 95382: contig of 4428 bp in length
95383 95482: gap of 100 bp
95483 99003: contig of 3521 bp in length.

FEATURES

source

misc_feature
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fragment_chain:1"
2914..7380
/note="assembly_fragment:00288
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7481..11099
/note="assembly_fragment:00866
fragment_chain:1"
11200..13897
/note="assembly_fragment:00009
fragment_chain:2"
13998..16453
/note="assembly_fragment:01072
fragment_chain:2"
16554..19055
/note="assembly_fragment:00251
fragment_chain:3"
19156..21888
/note="assembly_fragment:00690
fragment_chain:3"
21989..25542
/note="assembly_fragment:00425
fragment_chain:4"
25643..30331
/note="assembly_fragment:01070
fragment_chain:4"
30432..32487
/note="assembly_fragment:00445
fragment_chain:5"
32588..36034
/note="assembly_fragment:00608
fragment_chain:5"
36135..38214
/note="assembly_fragment:00916
fragment_chain:6"
38315..40332
/note="assembly_fragment:00154
fragment_chain:6"
40433..43002
/note="assembly_fragment:00962
fragment_chain:7"
43103..48212
/note="assembly_fragment:00891
fragment_chain:7"
48313..52476
/note="assembly_fragment:01004
fragment_chain:8"
52577..54653
/note="assembly_fragment:01069

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misc_feature      fragment_chain:8"
54734..57605
/Note="assembly-fragment:00023"
misc_feature      57706..60028
/Note="assembly-fragment:00102"
misc_feature      60129..63554
/Note="assembly-fragment:00233"
misc_feature      63655..66479
/Note="assembly-fragment:00295"
misc_feature      66580..72814
/Note="assembly-fragment:00378"
misc_feature      72915..78995
/Note="assembly-fragment:00427"
misc_feature      79096..82552
/Note="assembly-fragment:00693"
misc_feature      82653..85473
/Note="assembly-fragment:00752"
misc_feature      85574..88078
/Note="assembly-fragment:00834"
misc_feature      88179..90954
/Note="assembly-fragment:00887"
misc_feature      91055..95382
/Note="assembly-fragment:00939"
misc_feature      95483..99003
/Note="assembly-fragment:01026"
BASE COUNT      24057 a 23751 c 23770 g 24578 t 2847 others
ORIGIN

```

```

Query Match      5.9% Score 122.6; DB 2; Length 99003;
Best Local Similarity 48.6% Pred. No. 2.3e-07;
Matches 368; Conservative 0; Mismatches 385; Indels 4; Gaps 2;

QY 194 ATGTATGAAATTTGATTTATGACACGTGTAAGAAAGTAAAGATTGTTGTTCTTTT 253
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 11088 ANNTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 11029
QY 254 TTTAAATTCAGATTAATTAATTTTGCAGAAATTTGCAAAATATCCATGTCGAAAT 313
DB 11028 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 10969
QY 314 AAATTTGAAAGCAAAATATCAACCTTTTGCAGACACTTTTACAAAAATCCAT 373
DB 10968 TTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 10909
QY 374 TTTGAGAAAAAATTTACATTAATTCGAAATCAAAATGCTATGAAAAATTTTAAA 433
DB 10908 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 10849
QY 434 TTTGCTTACCTTAATTAATGCAAACTGTTAAATTTAGAAAAAGAGAAAAATAAA 493
DB 10848 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 10789
QY 494 AAATGACATTTCAAGGAAATCAAAATGCTATGAAAAATTTTAAATTTTAAAT 553
DB 10788 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 10729
QY 554 ATAAATGAAATTCAGAGTGTAAATTTAGAAAAAGAGAAAAATTTAAATGACCATTTCA 613
DB 10728 AAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 10669
QY 614 TTCAA--AATCAGATTTGTTGTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 671
DB 10668 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 10609
QY 672 CAATGCTGAACATTTAGAAAAAGAGAAAAATTTAAATTTTAAATTTTAAATTTTAAATTT 731
DB 10608 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 10549
QY 732 ATTTGTAATTCAGATTTTGAAGTTAGACAGAAAAAATGCAATTTGCTTAACTT 791
DB 10548 ATTA--AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 10491

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QY 792 TTGCGTTACATTTTGGATCATAGAAATTAATTCATCAAAAACTATTATA 851
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 10490 AAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 10431
QY 852 AATTACAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 911
DB 10430 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 10371
QY 912 CATACGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 948
DB 10370 TATTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 10334

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RESULT 13
CEY53C12D/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

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JOURNAL
MEDLINE
REMARK
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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Genome sequence of the nematode *C. elegans*: a platform for investigating biology. The *C. elegans* Sequencing Consortium
 Submitted (02-NOV-1998) Nematode Sequencing Project, Sanger Centre,
 Hinxton, Cambridge CB10 1HQ, England and Department of Genetics,
 Washington University, St. Louis, MO 63110, USA. E-mail:
 jess@anger.ac.uk or fw@nematode.wustl.edu
 Coding sequences below are predicted from computer analysis, using
 predictions from GeneFINDER (P. Green, U. Washington), and other
 available information.
 Current sequence finishing criteria for the *C. elegans* genome
 sequencing consortium are that all bases are either sequenced
 unambiguously on both strands, or on a single strand with both a
 dye primer and dye terminator reaction, from distinct subclones.
 Exceptions are indicated by an explicit note.
 IMPORTANT: This sequence is not the entire insert of clone Y53C12D.
 It may be shorter because we only sequence overlapping sections
 once, or longer because we arrange for a small overlap between
 neighbouring submissions.
 The start of this sequence (1..117) overlaps with the end of
 sequence Y99277.
 The end of this sequence (1390..1496) overlaps with the start of
 sequence Y99278.
 For a graphical representation of this sequence and its analysis
 see: - [http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?](http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=Y53C12D)
 name=Y53C12D.

FEATURES
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 Location/Qualifiers
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 /db_xref="taxon:6239"
 /chromosome="II"
 /clone="Y53C12D"

BASE COUNT 607 a 92 c 94 g 703 t

ORIGIN

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Query Match      5.8% Score 121.6; DB 3; Length 1496;
Best Local Similarity 47.7% Pred. No. 5.5e-07;
Matches 481; Conservative 0; Mismatches 519; Indels 8; Gaps 4;

QY 55 TCTTTTAATCTTCAAGTATTTTACATTAATGAGCTATTTGTGAGTGAAGAAATGAG 114
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT	15
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LOCUS	PMAL3P7 253305 bp DNA INV 22-MAY-2000
DEFINITION	Plasmidom falciparum MAL3P7, complete sequence.
ACCESSION	AF034559 AF008974 AL0008975 AL0008981 AL000983 AL010138 AL010143 AL010146 AL010154 AL010157 AL010160 AL010165 AL010169 AL010187 AL010189 AL010207 AL010208 AL010214 AL021885 AL021888 AL139179 Z98556 Z98557 Z98558
VERSION	AL034559.4 GI:8052273
KEYWORDS	Htg; 40S Ribosomal protein S3a; acyl transferase; acylaminoacyl-peptidase; Arg-dependent RNA Helicase; cyclophilin; elongation factor; F49G12.11-like protein; Hesp-like domain protein; histone H2A variant; kinesin-related protein; N-acetylglucosamine-1-phosphate phosphatase; protein kinase; R-CG repeat; R-FR3 repeat; rep11; rep20; tiffin; RNA-binding protein; stevor; T-complex protein I epsilon subunit; telomere; var. malaria parasite P. falciparum.
SOURCE	Plasmidom falciparum
ORGANISM	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE	1 (bases 1 to 253305)
AUTHORS	Boman,S., Lawson,D., Basham,D., Brown,D., Chillingworth,T., Churcher,C.M., Craig,A., Davies,R.M., Devlin,K., Felwell,T.,

FEATURES	source	gene	CDS	misc_feature
TITLE				
JOURNAL				
REFERENCE				
AUTHORS				
JOURNAL				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
FEATURES				
source				
gene				
CDS				
misc_feature				

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misc_feature
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/gene="PFC0865w, MAL3p7.2"
/note="PFC0865w, MAL3p7.2", RNA-binding protein, len: 309
aa: Similarity eg to C.elegans RNA-binding protein (TR:Q18318) BLAST Score: 378, sum P(1) = 3.8e-35; 378 identity in 287 aa overlap, predicted using hexexon, pfam: match to PF0076 rrm, RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) Score 58.01"
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/note="PFC0870w, MAL3p7.3", putative elongation factor,
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1-beta. (AAF27524) (276 aa), fasta scores: opt: 366, E():
1.1e-15, 53.28 identity in 141 aa overlap, revised:
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guanine nucleotide exchange domain Score 61.10"
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end"
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Query Match
Best Local Similarity 5.8%; Score 121.6; DB: Length 253305;
Pred. No. 2,7e-07;
Matches 444; Conservative 0; Mismatches 484; Indels 12; Gaps 2;

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QY 141 TTTATATTAATTGACCTTAATTGATTCATTTTCATATATCTGAACAGAGTATGATG 200
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Db 222931 TTTTATATTTTGAAGTATATATATATAGTGATATATATATATATATGTTGTG 222872

QY 201 AAATTGATTCATTTATGACACTGATGAAAGTAAAGATTAAGATTACTTTTAAAAA 260
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 222871 TATATGATGTTGTTGATGTTGATGATATATATATATATATATATATATATAT 222812

QY 261 TTCCATATTAATTTTGGCCAAACTTTTGCATAATATCATGTTCCGAATAATATTT 320
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 222811 ATTTATATATATATATATATATATATATATATATATATATATATATATATAT 222752

QY 321 GAAAAACAAACAAATATCAAACTTTTGGCAACACTTTTACAAAATTCATTTTACA 380
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 222751 GAAAAATGAAATATATAAAAAATTTATTAATAAAAAAAGAAAAAAGAAAAAGA 222692

QY 381 AAAAAAATTTACATTAACCTTGC-----AAATCAAAATTTGATGAAAAATTTAA 431
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 222691 AAAATATTTTAAATATATATAAAATTTATATATATATATATATATTTGTTAAAA 222632

QY 432 AATTTCCCTTTCACCTATATATGAAGCTCAAGCTGTTAAATTTAGAAAGAGAAAAATA 491
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 222631 TGAAAAATATATATCAAAAAAATTAATAAAAAAATTTATATATAAAAAACAATGATATA 222572

QY 492 AAAATGACATTTTCATGCGAAATGCAATTTGATGAAAAACTTAAATTTTATTTTAA 551
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 222571 AAAAAATTTTATTTACATATAAAAAAAGAAAAAAGAAAAAAGAAAAAATTTATATA 222512

QY 552 ATATATATGAATTTCAAGGTGTTAAATTTAGAAAGAGCAAAATTAATAATGACATTT 611
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 612 CATTCAAATACAGATTGTGATGAAAAATTTAAATTTTATTCAAATATATATGAAACT 671
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Db	222451	AAAAAAAAAATTTATTTAAATAAAAAATAAAAAATTTAAATTTAATTAATTAATAA	222392
QY	672	CAAAAGTGACATTATGAAAAGAGAAAAATTTAAATGATGAAATTTGTAAACATCA	731
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QY	732	ATTGTGAATTCACAATTTGAAAGTTGACACAGAAAAAATCGAATGTCCTATAC	791
Db	222334	AAAAATAAAAAATTTATTTAAATAAAAAATAAAAAATTTGAATTTAAATAAAAA	222275
QY	792	TTGCGTTACATTTTGGGATCATAAAGAAATACGTGAATTCATTCAAAACTATT	851
Db	222274	AAAAATAAAAATTTAAATTAATAAAAAAATAAAAAATTTAAATTAATACATGCAATAT	222215
QY	852	AATTTCAAAAATGAAATTAACCAAAAAAAGAGAGACATGACGATTTCTGTAAGAAC	911
Db	222214	ACATACATATATATACATATTATATATATATATATATATATATATATATATATAT	222155
QY	912	CATACGTGATTTAAAGACATCGCATATTAGAAATGAGAAAAAATAAACTATT	971
Db	222154	TACAT	222095
QY	972	TCACAAAAATGATTAACACATCAAAAGAACATGAAGAAATCTTATTCACAAAAATG	1031
Db	222094	TCATATATATATCCTAAGACATATATATATATATATATATATATATATATATAT	222035
QY	1032	TGAAGTTAAATACATGATTCATTTGATTTATTTACTA	1071
Db	222034	TAAATATATACATACACATATATATGCTCTTTTTTTTTTA	221995

Search completed: February 23, 2002, 08:50:12
Job time: 12875 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 23, 2002, 06:33:03 ; Search time 121.84 Seconds

(without alignments)
14706.252 Million cell updates/sec

Title: us-09-636-826-1

Perfect score: 2090

Sequence: 1 GATATCACACATTCGTCAT.....TCGCTTTCGCTCTCTCT 2090

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

N_Geneseq_1101:*

- 1: /SIDS2/gcgdata/geneseq/NA1980.DAT.*
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- 21: /SIDS2/gcgdata/geneseq/NA2000.DAT.*
- 22: /SIDS2/gcgdata/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2090	100.0	2090	22	AA61197
2	266	12.7	936	22	AA61197
3	266	12.7	936	22	AA61197
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5	266	12.7	936	22	AA61197
6	266	12.7	936	22	AA61197
7	266	12.7	936	22	AA61197
8	264.6	12.7	936	22	AA61197
9	264.6	12.7	936	22	AA61197
10	264.6	12.7	936	22	AA61197
11	264.6	12.7	936	22	AA61197

12	264.6	12.7	936	22	AA61197	Oligonucleotide D2
13	264.6	12.7	936	22	AA61197	Oligonucleotide D1
14	131	6.3	6644	20	AA61197	Base sequence of t
15	131	6.3	7372	20	AA61197	Base sequence of t
16	131	6.3	7797	20	AA61197	Base sequence of t
17	131	6.3	7996	20	AA61197	Base sequence of t
18	105.4	5.0	1035	21	AA61197	Base sequence of t
19	101	4.8	9789	17	AA61197	Human colon cancer
20	97	4.6	19124	18	AA61197	Plasmodium var-7 p
21	97	4.6	19124	21	AA61197	Plasmodium var-7 p
22	91.4	4.4	6033	21	AA61197	Plasmodium var-7 p
23	89.6	4.3	335913	22	AA61197	Plasmodium var-7 p
24	89.6	4.3	335913	22	AA61197	Plasmodium var-7 p
25	88	4.2	875	21	AA61197	Plasmodium var-7 p
26	87.6	4.2	6042	21	AA61197	Plasmodium var-7 p
27	86.6	4.2	8310	20	AA61197	Plasmodium var-7 p
28	86.6	4.1	10640	22	AA61197	Plasmodium var-7 p
29	86.2	4.1	2503	15	AA61197	Plasmodium var-7 p
30	85.2	4.1	4041	21	AA61197	Plasmodium var-7 p
31	84.4	4.0	244	22	AA61197	Plasmodium var-7 p
32	84	4.0	1132	21	AA61197	Plasmodium var-7 p
33	83.4	4.0	244	22	AA61197	Plasmodium var-7 p
34	82.8	4.0	1527	21	AA61197	Plasmodium var-7 p
35	81.6	3.9	26811	20	AA61197	Plasmodium var-7 p
36	80.2	3.8	700	22	AA61197	Plasmodium var-7 p
37	79.2	3.8	20674	21	AA61197	Plasmodium var-7 p
38	79	3.8	111309	20	AA61197	Plasmodium var-7 p
39	78.8	3.8	3101	11	AA61197	Plasmodium var-7 p
40	78.8	3.8	5139	21	AA61197	Plasmodium var-7 p
41	78.4	3.8	1612	7	AA61197	Plasmodium var-7 p
42	78	3.7	910715	20	AA61197	Plasmodium var-7 p
43	77.6	3.7	1671	13	AA61197	Plasmodium var-7 p
44	77.4	3.7	5454	21	AA61197	Plasmodium var-7 p
45	77.4	3.7	5940	21	AA61197	Plasmodium var-7 p

ALIGNMENTS

RESULT 1

AA61197 standard; DNA; 2090 BP

AA61197:

23-MAR-2001 (first entry)

B. vulgaris V-ATPase subunit C isoform 2 promoter DNA.

Promoter: V-ATPase; subunit C; isoform 2; plant; transgenic plant;

V-type adenosine triphosphatase; stress resistance; insect resistance;

herbicide resistance; disease resistance; salt stress; constitutive;

nutrient deficiency; injury; infection; selection marker; ss.

Beta vulgaris.

WO200114572-A2.

01-MAR-2001.

10-AUG-2000; 2000WO-EP07774.

26-AUG-1999; 99DE-1040648.

26-AUG-1999; 99US-0150867.

(BADI) BASF AG.

Duvenig E, Rauch T;

WPI: 2001-218455/22.

New DNA construct containing a plant V-type adenosine triphosphatase promoter, useful for recombinant protein expression or producing

QY 1621 AACTATGTTGCTCACCCCTTAAGATGATATGTAATAAACCCTGAGGCTTTGGCTTAA 1680
 Db 1621 aactatgttgcctcaccccttaagatgatatgttaaaccttgaagtggcttggcttaa 1680
 QY 1681 AAAAGTCCACCAAGCCCAATTTAGCTCCCAAAACCCAGCAAAATTTCTGGTACTAT 1740
 Db 1681 aaaagtcacccaagcccaattctagctcccaaacacgaatttcttgtaactat 1740
 QY 1741 CCAAAACAAAACAAACACCTCTGATCAACCAAGAAAATTAATTAATTTTGTGTTT 1800
 Db 1741 ccaaaacaaaacaaacacccctctgatacaccagaaaaataacatatttctgttt 1800
 QY 1801 CTCCTCAATTTTCAATTTTATTTATCAGCGAAGATACATTAATTAATCAAGGTA 1860
 Db 1801 ctcccaatttctcaatttaattatcaagggaaagtaacataatcaacaaaggtaa 1860
 QY 1861 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1920
 Db 1861 aaaaaataaataaataaataaataaataaataaataaataaataaataaataaataa 1920
 QY 1921 CTCATATTTTCATCAACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1980
 Db 1921 ctcataatttcacacgcctctctctctctctctctctctctctctctctctctcaga 1980
 QY 1981 TCGATTCAGCAATTCATCAACACCTTCGATCATCAACATCAAAAAATGTCACAG 2040
 Db 1981 tcggttaagcaattcatcagaaacaccttcgcgataccacacaaataaataaataaag 2040
 QY 2041 TCTTTAAGCGGATGAACGCGCGCTTCTTGGCTTTCTGGTGGTGGTGGTGGTGGT 2090
 Db 2041 tctttaacgagatgaacgagcgcttctctctctctctctctctctctctctctctct 2090

RESULT 2

AAF58252/C
 ID AAF58252 standard; DNA; 936 BP.

AC AAF58252;

XX 24-APR-2001 (first entry)

DE Oligonucleotide D1835.

XX Electron-transfer group; EFM; mismatch; genotyping;

KW gene expression; ss.

XX Synthetic.

PN WO200107665-A2.

PD 01-FEB-2001.

PF 26-JUL-2000; 2000WO-US20476.

PR 26-JUL-1999; 9905-0145695.

PR 17-MAR-2000; 2000US-0190259.

XX (CLIN-) CLINICAL MICRO SENSORS INC.

PI Unek RM;

DR WPI; 2001-159728/16.

PT Nucleic acids containing electron-transfer group, useful as labels in
 PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
 PT a single surface

PS Example 6; Page 127; 159pp; English.

CC The present invention relates to a composition comprising two nucleic
 CC acids each containing an electron-transfer group (ETM) having
 CC different redox potentials. The invention is used for electronic
 CC detection of nucleic acids, especially of substitutions (mismatches)

CC and single-nucleotide polymorphisms, e.g. for genotyping,
 CC monitoring gene expression.
 XX
 SQ Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;

Query Match 12.7%; Score 266; DB 22; Length 936;
 Best Local Similarity 0.6%; Pred. No. 1.4e-31;
 Matches 5; Conservative 607; Mismatches 172; Indels 0; Gaps 0;

QY 106 AAAATGGAGATATAGGATATAGTGAAGAGGCTTTATATATATTAAGCTTAATTTGA 165
 Db 787 WW 728
 QY 166 TTCAATTTTCATATCTGAAAACAGGTATGTAATTAATTAATTTGCTTATGACTGA 225
 Db 727 WW 668
 QY 226 TGAATAAGTTACGATTTAGTCTTTTAAATTCATTAATTAATTTTGCCCAAA 285
 Db 667 WW 608
 QY 286 CTTTGGAAAATATCCATGTTCCGAATTAATTTTGAATAACCAATATCAACCTT 345
 Db 607 WW 548
 QY 346 TTTGCAACAACCTTTTCAAAAATTCATTTGAGAAAAAAATTTACATTAACCTTGC 405
 Db 547 WW 488
 QY 406 AATCAATTTGTATGAAAATTTAAATTTCTTACCTATATATTAATCAACGTAAGT 465
 Db 487 WW 428
 QY 466 TTTAAATTTTGAAGAGAGAAAATTAATGACATTTTCATGCAATCAATTTGTGT 525
 Db 427 WW 368
 QY 526 ATGAAAACCTTAATTTTATTTAAATTAATTAATTTCAAAAGTCTTAATTTAGAA 585
 Db 367 WW 308
 QY 586 AAGAGAAAATTAATTAATGACATTTTCATTAATTAATTAATTTGATGAAAATTTAA 645
 Db 307 WW 248
 QY 646 TTTTATTTCAATTAATTTGAACCTCAAGTGAACATTTAGAAAAGAGAAAATTTA 705
 Db 247 WW 188
 QY 706 AATGATGAAAATTTTGAATAACATCAATTTGGAATGCAATTTAGAACTGAGCAAG 765
 Db 187 WW 128
 QY 766 AAAAAAACTGATTTGCTTATTTGCTTATTAATTTTGGATCAATTAAGAAATTAC 825
 Db 127 WW 68
 QY 826 TGAATCCATATCAAAACTATTTATTAATTTACAAAAATGAATTAACAAAAAGAAGA 885
 Db 67 WW 8
 QY 886 ACAT 889
 Db 7 WWWWW 4

RESULT 3

AAF58254/C
 ID AAF58254 standard; DNA; 936 BP.

AC AAF58254;

XX

DT 24-APR-2001 (first entry)
 XX Oligonucleotide D1875.
 DE Electron-transfer group; ETM; mismatch; genotyping;
 KW gene expression; ss.
 XX Synthetic.
 OS
 XX MO200107665-A2.
 PN
 XX 01-FEB-2001.
 PD
 XX 26-JUL-2000; 2000WO-US20476.
 PF
 XX 26-JUL-1999; 99US-0145695.
 PR 17-MAR-2000; 2000US-0190259.
 XX
 XX (CLIN-) CLINICAL MICRO SENSORS INC.
 PA
 XX
 XX Umek RM:
 PI
 XX WPI; 2001-159728/16.
 DR
 XX Nucleic acids containing electron-transfer group, useful as labels in
 PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
 PT a single surface -
 XX
 XX Example 6; Page 127; 159pp; English.
 PS
 XX The present invention relates to a composition comprising two nucleic
 CC acids each containing an electron-transfer group (ETM) having
 CC different redox potentials. The invention is used for electronic
 CC detection of nucleic acids, especially of substitutions (mismatches)
 CC and single-nucleotide polymorphisms, e.g. for genotyping,
 CC monitoring gene expression.
 XX
 XX Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
 SQ
 Query Match 12.7%; Score 266; DB 22; Length 936;
 Best Local Similarity 0.6%; Pred. No. 1.4e-31;
 Matches 5; Conservative 607; Mismatches 172; Indels 0; Gaps 0;

DB 367
 QY 586 AAGGAGAAAAATTAAATGACCATTTCTCAAAATCAGATGCTGATGAAAAATTTAA 645
 DB 307
 QY 646 TTTTATTTTCAATATATATGAACTCAAGCTGGAACATTTGAAAGAGAAAAATTA 705
 DB 247
 QY 706 AATGATGAAAAATTGTAATCAATTCATTTGTGAATCAGAAATTAGACAGTACAGAG 765
 DB 187
 QY 766 AAAAAAAGTGAATGCTTACTTTTCGTTACAAATTTGGGATCATAGAAATTTAC 825
 DB 127
 QY 826 TGAATTCATATCAAAACCTATTAAATTACAAAAATGATAAACCAGAAAAAGAGA 885
 DB 67
 QY 886 ACAT 889
 DB 7
 QY 886 ACAT 889
 DB 7
 RESULT 4
 AAF58257/c
 ID AAF58257 standard; DNA; 936 BP.
 AC AAF58257;
 AC 24-APR-2001 (first entry)
 DT
 XX Oligonucleotide D1954.
 DE
 XX Electron-transfer group; ETM; mismatch; genotyping;
 KW gene expression; ss.
 XX
 XX Synthetic.
 OS
 XX MO200107665-A2.
 PN
 XX 01-FEB-2001.
 PD
 XX 26-JUL-2000; 2000WO-US20476.
 PF
 XX 26-JUL-1999; 99US-0145695.
 PR 17-MAR-2000; 2000US-0190259.
 XX
 XX (CLIN-) CLINICAL MICRO SENSORS INC.
 PA
 XX
 XX Umek RM:
 PI
 XX WPI; 2001-159728/16.
 DR
 XX Nucleic acids containing electron-transfer group, useful as labels in
 PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
 PT a single surface -
 XX
 XX Example 6; Page 127; 159pp; English.
 PS
 XX The present invention relates to a composition comprising two nucleic
 CC acids each containing an electron-transfer group (ETM) having
 CC different redox potentials. The invention is used for electronic
 CC detection of nucleic acids, especially of substitutions (mismatches)
 CC and single-nucleotide polymorphisms, e.g. for genotyping,
 CC monitoring gene expression.
 XX
 XX Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;

Query Match 12.7%; Score 266; DB 22; Length 936;
 Best Local Similarity 0.6%; Pred. No. 1.4e-31;
 Matches 5; Conservative 607; Mismatches 172; Indels 0; Gaps 0;

```

QY 106 AAAATGGAGATATAGCAATAGTTGAAAAGGCTTTATATATATAGACTTAATTTGA 165
DB 787 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 728
QY 166 TTCAATTCATATACGTAAACAAGATGATGATGAATTTGATTCATTTATGACACTGA 225
DB 727 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 668
QY 226 TGAAGAAGTTAAGCATTTAGTTCTTTTAAAAATTCATTAATTAATTTTGGCCAAA 285
DB 667 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 608
QY 286 CTTTGGCAAAATATCATGTTGCGAAATTAATTTGAAAAACAACATATCAACCTT 345
DB 607 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 548
QY 346 TTTCGGAACAACCTTTTCAAAAATCCATTTTCAGAAAAAAATTTACATTAATTCGCA 405
DB 547 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 488
QY 406 AATCAATTTGTATGAAAAATTTAAATTTCCCTTTCACCTATATTAATGAACTCAAGTG 465
DB 487 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 428
QY 466 TTAATAATTTAGAAAGAGAAAAATAAAATGACCATTTTCAGCAATTCATTAATTTGT 525
DB 427 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 368
QY 526 ATGAAAACTTAATTTTATTTTAAATATATGAAATCAAGTGTAAATTTAGAA 585
DB 367 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 308
QY 586 AAGGAGAAAAATTAATGACCATTTTCATTAATGATGATGATGAAAAATTTAA 645
DB 307 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 248
QY 646 TTTTATTTCAATATATATTGAAAGTCAAGTGTGAACATTTGAAAAAGAGAAAAATTA 705
DB 247 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 188
QY 706 AATGATGAAAAATTTGTAACAATCAATTTGTGAATCAGATTTTGAAGTTGACAGAG 765
DB 187 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 128
QY 766 AAAAAAAGTGAATTTCTTATCTTTTGGTACAAATTTTGGATCATTAAGAAATTAAC 825
DB 127 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 68
QY 826 TGAATGCATATCAAAAACATATATTAATTTACAAAAATGATTAACCAAAAAACAAGA 885
DB 67 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 8
QY 886 ACAT 889
DB 7 WWWW 4

RESULT 5
ID AAF58259/c
XX AAF58259 standard; DNA; 936 BP.
XX AC
XX AAF58259;
XX 24-APR-2001 (first entry)
XX Oligonucleotide D2004.
XX DE
XX Electron-transfer group; ETM; mismatch; genotyping;
  
```

KM gene expression; ss.
 XX Synthetic.
 OS WO200107665-A2.
 PN 01-FEB-2001.
 PD 26-JUL-2000; 2000WO-US20476.
 XX 26-JUL-1999; 99US-0145695.
 XX 17-MAR-2000; 2000US-0190259.
 PA (CLIN-) CLINICAL MICRO SENSORS INC.
 PI Dmek RM;
 DR WPI; 2001-159728/16.
 XX
 PT Nucleic acids containing electron-transfer group, useful as labels in
 PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
 PT a single surface
 XX
 PS Example 6; Page 128; 159pp; English.
 XX
 CC The present invention relates to a composition comprising two nucleic
 CC acids each containing an electron-transfer group (ETM) having
 CC different redox potentials. The invention is used for electronic
 CC detection of nucleic acids, especially of substitutions (mismatches)
 CC and single-nucleotide polymorphisms, e.g. for genotyping,
 CC monitoring gene expression.
 XX
 SQ Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;

Query Match 12.7%; Score 266; DB 22; Length 936;
 Best Local Similarity 0.6%; Pred. No. 1.4e-31;
 Matches 5; Conservative 607; Mismatches 172; Indels 0; Gaps 0;

```

QY 106 AAAATGGAGATATAGCAATAGTTGAAAAGGCTTTATATATATAGACTTAATTTGA 165
DB 787 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 728
QY 166 TTCAATTCATATACGTAAACAAGATGATGATGAATTTGATTCATTTATGACACTGA 225
DB 727 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 668
QY 226 TGAAGAAGTTAAGCATTTAGTTCTTTTAAAAATTCATTAATTTTGGCCAAA 285
DB 667 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 608
QY 286 CTTTGGCAAAATATCATGTTGCGAAATTAATTTGAAAAACAACATATCAACCTT 345
DB 607 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 548
QY 346 TTTCGGAACAACCTTTTCAAAAATCCATTTTCAGAAAAAAATTTACATTAATTCGGA 405
DB 547 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 488
QY 406 AATCAATTTGTATGAAAAATTTAAATTTCCCTTTCACCTATATTAATGAACTCAAGTG 465
DB 487 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 428
QY 466 TTAATAATTTAGAAAGAGAAAAATAAAATGACCATTTTCAGCAATTCATTAATTTGT 525
DB 427 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 368
QY 526 ATGAAAACTTAATTTTATTTTAAATATATGAAATCAAGTGTAAATTTAGAA 585
DB 367 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 308
QY 586 AAGGAGAAAAATTAATGACCATTTTCATTAATGATGATGATGAAAAATTTAA 645
  
```

QY	106	AAATGAGATAAATAGCAATTAGTTCGAAAAGGGGTATATATATATGAGCTTAATTTGA	1655
Db	787	AA	728
QY	166	TTCAATTTCATATATCTGAAAACAAGTATGATGAAATTTGATTCATTTATGACACTGA	225
Db	727	AA	668
QY	226	TGAAAAAGTTACGATTTAGTCTCTTTTAAAAATTCACATATAAATTTTGCCAAA	285
Db	667	AA	608
QY	286	CTTTTGCAGAAATATCCATGTTCCGAAATAAATTTGAAAAACAAACATATCAACCTT	345
Db	607	AA	548
QY	346	TTTCGAGCACTTTTACAAAATCCATTTTCAGAAAAAAAATTTACATTAACCTTCGA	405
Db	547	AA	488
QY	406	AATCAAAATGTGTATGAAAAATTTAAAAATTTCTTTCACCATATATTTGAAACTCAAGTG	465
Db	487	AA	428
QY	466	TTAAAATTTAGAAAAGAGAAAAATPAAAAATGCACATTTTCATGCGAAATCAATTGTGT	523
Db	427	AA	368
QY	526	ATGAAAAACTTAAATTTTATTTAAATATATATGAAATTCAGATTCAGATTTTAAATTTGAA	585
Db	367	AA	308
QY	586	AAGGAGAAAAATTAATGACCATTTTCATTCAGAAATCAGATTTGTATGAAAAATTTAAA	645
Db	307	AA	248
QY	646	TTTTTATTTCAATATATATTAATTTGAACTCAAGTGTGACATTTTACAAAAGGAAAAATTA	705
Db	247	AA	188
QY	706	AAATGATGAATATTTGTAAAAACATCAATTTTGAAATCAGAAATTTAGAGTTACACAAG	765
Db	187	AA	128
QY	766	AAAAAAAACGTGATTTGTCTTACTTTTCGTTACATTTTGGCATCATATAAGAAATTAC	822
Db	127	AA	68
QY	826	TGAATTCATATCAAAAACCTATTTAATTTCAAAAATGATTAACCAAAAAGAGAGA	885
Db	67	AA	8
QY	886	ACAT 889	
Db	7	AAAA 4	
RESULT 7			
AAFS8255/c			
ID AAF88255 standard; DNA; 938 BP.			
XX AAF58255;			
XX			
DT 24-APR-2001 (first entry)			
XX			
XX Oligonucleotide D1876.			
XX			
XX Electron-transfer group; ETM; mismatch; genotyping;			
XX gene expression; ss...			
XX			
OS Synthetic.			
XX			
PN WO200107665-A2.			

XX 01-FEB-2001.
 PD
 XX 26-JUL-2000; 2000WO-US20476.
 PF
 XX 26-JUL-1999; 99US-0145695.
 PR
 XX 17-MAR-2000; 2000US-0190259.
 XX
 PA (CLIN-) CLINICAL MICRO SENSORS INC.
 XX
 PI umek RM;
 DR WPI: 2001-159728/16.
 XX
 XX Nucleic acids containing electron-transfer group, useful as labels in
 PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
 PT a single surface
 XX
 PS Example 6; Page 127; 159pp; English.
 XX
 CC The present invention relates to a composition comprising two nucleic
 CC acids each containing an electron-transfer group (ETW) having
 CC different redox potentials. The invention is used for electronic
 CC detection of nucleic acids, especially of substitutions (mismatches)
 CC and single-nucleotide polymorphisms, e.g. for genotyping,
 CC monitoring gene expression.
 XX
 SQ Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;

Query Match 12.7%; Score 266; DB 22; Length 938;
 Best Local Similarity 0.6%; Pred. No. 1.4e-31;
 Matches 5; Conservative 607; Mismatches 172; Indels 0; Gaps 0;

QY 106 AAATGGAGTAATAGCAATAGTGAAGAGGTTTATTAATTAAGACTTAATTTGA 165
 DB 787 WWWWWW
 QY 166 TTCAATTCATATCTGAACAAGTATGTAATTTGATTCAATTTATGACACTGA 225
 DB 727 WWWWWW
 QY 226 TGAAGAACTTAAGATTAGTCTTTTAAATTCATTAATTAATTTTCCCAAAA 285
 DB 667 WWWWWW
 QY 286 CTTTGCAAAATATCCATGTCGAAATTAATTTGAAAACCAATATCAACCTT 345
 DB 607 WWWWWW
 QY 346 TTTCGCAACAATTTTCAAAAATCCATTTTCAGAAAAAAATTTGATTACTTCCGA 405
 DB 547 WWWWWW
 QY 406 AATCAATTTGTATGAATAATTTAAATTTCTTCACCTATATTAATGAACCTCAAGTG 465
 DB 487 WWWWWW
 QY 466 TTAATAATTTGAAGAGGAGAAAAATATAATGACATTTTCAGCGAAATCAATTTGTGT 525
 DB 427 WWWWWW
 QY 526 ATGAAAACTTAATAATTTTAAATTAATTAATTAATGAATCAAGTGAATTTAGAA 585
 DB 367 WWWWWW
 QY 586 AAGGAGAAATTAATTAATGACATTTTCATTAATTAATTAATTAATTAATTAATTA 645
 DB 307 WWWWWW
 QY 646 TTTTATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 705
 DB 247 WWWWWW

QY 706 AAATGATGAATAATTTGTAACATCAATTTGTGAATTCAGAAATTTAGAGTACAGAG 765
 DB 187 WWWWWW
 QY 766 AAAAAACGATGCTCTTATATCTTTTCGTTTACATTTTGGGATCATTAAGAAATTAAC 825
 DB 127 WWWWWW
 QY 826 TGAATCCATATCAAAAACCTATTATTAATTAATTAATTAATTAATTAATTAATTA 885
 DB 67 WWWWWW
 QY 886 ACAT 889
 DB 7 WWWWWW

RESULT 8

AF58252
 ID AAF58252 standard; DNA; 936 BP.
 XX
 AC AAF58252;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Oligonucleotide D1835.
 XX
 KW Electron-transfer group; ETW; mismatch; genotyping;
 KM gene expression; ss.
 XX
 OS Synthetic.
 XX
 PN WO200107665-A2.
 PD 01-FEB-2001.
 XX
 PF 26-JUL-2000; 2000WO-US20476.
 PR 26-JUL-1999; 99US-0145695.
 PR 17-MAR-2000; 2000US-0190259.
 XX

PA (CLIN-) CLINICAL MICRO SENSORS INC.

PI umek RM;

DR WPI: 2001-159728/16.

PT Nucleic acids containing electron-transfer group, useful as labels in
 PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
 PT a single surface
 XX

PS Example 6; Page 127; 159pp; English.

CC The present invention relates to a composition comprising two nucleic
 CC acids each containing an electron-transfer group (ETW) having
 CC different redox potentials. The invention is used for electronic
 CC detection of nucleic acids, especially of substitutions (mismatches)
 CC and single-nucleotide polymorphisms, e.g. for genotyping,
 CC monitoring gene expression.
 XX

SQ Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;

Query Match 12.7%; Score 264.6; DB 22; Length 936;
 Best Local Similarity 0.8%; Pred. No. 2.3e-31;

Matches 6; Conservative 606; Mismatches 175; Indels 0; Gaps 0;

QY 115 AATATAGGAATAGTGAAGAGGTTTATTAATTAATTAATTAATTAATTAATTTTC 174
 DB 2 WWWWWW
 QY 175 AATATGCAAAAACAAGTATGTAATTTGATTCAATTTATGACACTGATGAAAAAGT 234

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Db 62 ..... 121
QY 235 TAAAGATTAGTCTTTTAAATCCATATTAATTTTGGCCAAACTTTGGCA 294
Db 122 ..... 181
QY 295 AATATCATGTTGGGAATTAATTTGAAAAACAAATATCAACCTTTTGGGAC 354
Db 182 ..... 241
QY 355 AACCTTACAAAATCCATTTTCAGAAAAAAATTTACTTACTTGGAAATCAAT 414
Db 242 ..... 301
QY 415 GTGATGAAAAATTTAAATTTCCCTTCACCTATTAATGAACTCAAGTTAAATTT 474
Db 302 ..... 361
QY 475 AGAAAAGAGAAAAATTAATTAATGACATTTTCATGCAATCAATTTGTATGAAAAAC 534
Db 362 ..... 421
QY 535 TTAAATTTTATTTAATTAATTAATGAAATGTAAGTTAAATTTAGAAAAAGAGAAA 594
Db 422 ..... 481
QY 595 AATTAATAATGACATTTTCATTAATCAATGATGTATGAAAAATTTAAATTTTATTT 654
Db 482 ..... 541
QY 655 CAATATATATGAAACCAAGTGTGAACATTTAGAAAAAGAGAAAAATTAATTAATGA 714
Db 542 ..... 601
QY 715 AAATTTGTAACATCAATTTTGAATTCAGAAATTTAGAAAGAGAAAAAAAC 774
Db 602 ..... 661
QY 775 TGAATGTCTTATCTTTGCGTTGACATTTTGGGATCATTAAGAAATTTCTGAATCCA 834
Db 662 ..... 721
QY 835 TATCAAAAACATTAATTAATTAACAAATGATTAACCAAAAAAGAGACATGACA 894
Db 722 ..... 781
QY 895 TATTTG 901.
Db 782 ..... 788

```

RESULT 9

AAFS8254

ID AAF58254 standard; DNA; 936 BP.

XX AAF58254;

XX 24-APR-2001 (first entry)

XX Oligonucleotide D1875.

XX Electron-transfer group; ETM; mismatch; genotyping;

XX gene expression; ss.

XX Synthetic.

XX W0200107665-A2.

XX 01-FEB-2001.

XX 26-JUL-2000; 2000WO-US20476.

```

PR 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000US-0190259.
XX (CLIN-) CLINICAL MICRO SENSORS INC.
XX Umek RM;
XX WPI: 2001-159728/16.
XX
XX Nucleic acids containing electron-transfer group, useful as labels in
XX hybridization assays, e.g. for genotyping, allowing repeat analyses on
XX a single surface
XX
XX Example 6; Page 127; 159pp; English.
XX
XX The present invention relates to a composition comprising two nucleic
XX acids each containing an electron-transfer group (ETM) having
XX different redox potentials. The invention is used for electronic
XX detection of nucleic acids, especially of substitutions (mismatches)
XX and single-nucleotide polymorphisms, e.g. for genotyping,
XX monitoring gene expression.
XX
XX Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other:

```

Query Match 12.7%; Score 264.6; DB 22; Length 936;

Best Local Similarity 0.8%; Pred. No. 2,3e-31;

Matches 6; Conservative 606; Mismatches 175; Indels 0; Gaps 0;

```

QY 115 AATATGAAATAGTTGAAAAGGTTTATATTAATTAAGCTTAATTTGATCATTTTC 174
Db 2 ..... 61
QY 175 ATATATCGAAAACAGTATGATGAAATTTGATTCATTTATGACACTGATGAAAAAGT 234
Db 62 ..... 121
QY 235 TAAAGATTAGTCTTTTAAATTTCAATATTAATTTTGGCCAAACTTTTGGCA 294
Db 122 ..... 181
QY 295 AATATCATGTTGGAATTAATTTTGA AAAACAAATATCAACCTTTTGGGAC 354
Db 182 ..... 241
QY 355 AACCTTTCAAAATCCATTTTCAGAAAAAAATTTCACTTACTTGGAAATCAATT 414
Db 242 ..... 301
QY 415 GTGATGAAAAATTTAAATTTCTTTCACCTATTAATGAAACTCAAGTGTAAATTT 474
Db 302 ..... 361
QY 475 AGAAAAGAGAAAAATTAATTAATGACATTTTCATGCAATCAATTTGTATGAAAAAC 534
Db 362 ..... 421
QY 535 TTAAATTTTATTTAATTAATTAATGAAATGTAAGTTAAATTTAGAAAAAGAGAAA 594
Db 422 ..... 481
QY 595 AATTAATAATGACATTTTCATTAATCAATGATGTATGAAAAATTTTAAATTTT 654
Db 482 ..... 541
QY 655 CAATATTAATTAATTAATTAATGACATTTTCAGAAAAAGGAAAAATTTAAATGATGA 714
Db 542 ..... 601
QY 715 AAATTTGTAACATCAATTTTGAATTCAGAAATTTAGAAATTTAGCAAGAAAAAAAC 774
Db 602 ..... 661

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QY 775 TGAATGCTTACTTTGCTTACAAATTTGGGATCATTAAGAAATTTACTGAATCCA 834
Db 662
QY 835 TATCAAAACATTTTAAATTAACAAAATTAAGAACCAAAAAAGAGACATGACGA 894
Db 722
QY 895 TATTCG 901
Db 782
RESULT 10
AAF58257
ID AAF58257 standard; DNA; 936 BP.
AC AAF58257;
XX 24-APR-2001 (first entry)
XX 24-APR-2001 (first entry)
XX Oligonucleotide D1954.
XX Electron-transfer group; ETM; mismatch; genotyping;
XX gene expression; ss.
XX Synthetic.
XX WO200107665-A2.
XX 01-FEB-2001.
XX 26-JUL-2000; 2000MO-US20476.
XX 26-JUL-1999; 99US-0145695.
XX 17-MAR-2000; 2000US-0190259.
XX (CLIN-) CLINICAL MICRO SENSORS INC.
XX time RM;
XX WPI: 2001-159728/16.
XX Nucleic acids containing electron-transfer group, useful as labels in
XX hybridization assays, e.g. for genotyping, allowing repeat analyses on
XX a single surface .
XX Example 6; Page 127; 159pp; English.
XX The present invention relates to a composition comprising two nucleic
XX acids each containing an electron-transfer group (ETM) having
XX different redox potentials. The invention is used for electronic
XX detection of nucleic acids, especially of substitutions (mismatches)
XX and single-nucleotide polymorphisms, e.g. for genotyping,
XX monitoring gene expression.
XX Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other:
Query Match 12.7%; Score 264.6; DB 22; Length 936.
Best Local Similarity 0.8%; Pred. No. 2.3e-31;
Matches 6; Conservative 606; Mismatches 175; Indels 0; Gaps 0;
QY 115 ATAATAGGAATAGTGAAGAGGTGTTATATATAGACTTAATTTGATTCATTTTC 174
Db 2 61
QY 175 ATATATCTGAAAACAGTATGATGAATTTGATTCATTTATGACACGATGAAAAAGT 234
Db 62 121
QY 235 TAAAGATTTAGTCTTTTAAATTCATATATAATTTTGCCCAAAACTTTTGCAA 294
Db 235 294

Db 122 181
QY 295 AATATCAGTTGGGAATTAATTTGAAAAACAAAACATATCAACCTTTTGGGAC 354
Db 182 241
QY 355 AACTTTTACAAAATGCATTTTCAGAAAAAAATTTACATTAACCTGGCAATCAAT 414
Db 242 301
QY 415 GTGATGAAAAATTTAAATTTCTTCACCTAATTAATGAACCTCAAGTGTAAATTT 474
Db 302 361
QY 475 AGAAAGAGAAAAATTAATAATGACATTTGATGGAATCAATTTGATGAAAAAC 534
Db 362 421
QY 535 TTTAAATTTTATTTTAAATATATTAATGAATTCAGAACTGTAAATTTAGAAAAAGAAA 594
Db 422 481
QY 595 AATTAATGACCATTTCAATTCAGAAATGATGTGATGAATAATTTAATTTATTT 654
Db 482 541
QY 655 CAATATTAATTTGAACCTCAAGTGTGACATTTAGAAAAGAGAAAAATTAATGATGA 714
Db 542 601
QY 715 AATTTTGTAAACATCAATTTGTGAATCAGAAATTTAGAGTAGCAAGAAAAAAC 774
Db 602 661
QY 775 TGAATGCTTACTTTGCTTACAAATTTGGGATCATTAAGAAATTTACTGAATCCA 834
Db 662 721
QY 835 TATCAAAACATTTTAAATTAACAAAATTAAGAACCAAAAAAGAGACATGACGA 894
Db 722 781
QY 895 TATTCG 901
Db 782
RESULT 11
AAF58259
ID AAF58259 standard; DNA; 936 BP.
AC AAF58259;
XX 24-APR-2001 (first entry)
XX Oligonucleotide D2004.
XX Electron-transfer group; ETM; mismatch; genotyping;
XX gene expression; ss.
XX Synthetic.
XX WO200107665-A2.
XX 01-FEB-2001.
XX 26-JUL-2000; 2000MO-US20476.
XX 26-JUL-1999; 99US-0145695.
XX 17-MAR-2000; 2000US-0190259.
XX (CLIN-) CLINICAL MICRO SENSORS INC.
XX

PI Umek RM;
 XX WPI: 2001-159728/16.
 DR Nucleic acids containing electron-transfer group, useful as labels in
 XX hybridization assays, e.g. for genotyping, allowing repeat analyses on
 PT a single surface -
 PS Example 6; Page 128; 159pp; English.
 XX
 CC The present invention relates to a composition comprising two nucleic
 CC acids each containing an electron-transfer group (ETM) having
 CC different redox potentials. The invention is used for electronic
 CC detection of nucleic acids, especially of substitutions (mismatches)
 CC and single-nucleotide polymorphisms, e.g. for genotyping,
 CC monitoring gene expression.
 XX
 SQ Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;

Query Match 12.7%; Score 264.6; DB 22; Length 936;
 Best Local Similarity 0.8%; Pred. No. 2.3e-31;
 Matches 6; Conservative 606; Mismatches 175; Indels 0; Gaps 0;

QY 115 ATATAGCAATTTGTTGAAAGGTTTATATATAGCTAAATTTGATTCATTTTC 174
 DB 2 WWWWWW 61
 QY 175 ATATATCTGAACAAGATGATGTAATTTGATTCATTTAGACATGATGAAAAAGT 234
 DB 62 WWWWWW 121
 QY 235 TAACGATTAGTCTTTTAAATTCATATATATTTTGGCCAAACTTTGGCA 294
 DB 122 WWWWWW 181
 QY 295 AATATCATGTGCAATATAATTTGAAAAACAACAATATCAAACTTTTGGCAAC 354
 DB -182 WWWWWW 241
 QY 355 AACTTTACAAAAATTCATTTTCAGAAAAAAATTTACATTACTTGGCAATCAAAAT 414
 DB 242 WWWWWW 301
 QY 415 GTGATGAAAAATTTAAATTTCTTCACTTAATTTGAACCAAGTGTAAATTT 474
 DB 302 WWWWWW 361
 QY 475 AGAAAGGAGAAAAATATAAATGACATTTTCATGCAAAATCAAAATTTGTATGAAAAAC 534
 DB 362 WWWWWW 421
 QY 535 TTAATAATTTTAAATATAATTTGAATTTCAAGTGTAAATTTAGAAAAAGGAAA 594
 DB 422 WWWWWW 481
 QY 595 AATTAATAATGACATTTTCATCAAAATCAGATTTGTATGAAAAATTTAAATTTTATTT 654
 DB 482 WWWWWW 511
 QY 655 CAATATATATTTGAAGTCAAGTGTGAACATTTAGAAAAAGGAAAAATTTAAATGATGA 714
 DB 542 WWWWWW 601
 QY 715 AAATTTGTAACAATTTTGAATTCAGAAATTTGAAGTTAGACAGAAAAAAAC 774
 DB 602 WWWWWW 661
 QY 775 TGAATTTGCTATCTTTTGGTTCATATTTTGGATCATAAAGAAATTTCTGAAATCA 834
 DB 662 WWWWWW 721
 QY 835 TATCAAAAACTATTATATATACAAAAATGAATAAAAAGAAAAAGAACATGACGA 894

DB 722 WWWWWW 781
 QY 895 TATTTGCG 901
 DB 782 WWWWWW 788

RESULT 12

AAFS8262
 ID AAF58262 standard; DNA; 936 BP.
 AC AAF58262;
 DT 24-APR-2001 (first entry)
 DE Oligonucleotide D2007.
 XX
 KM Electron-transfer group; ETM; mismatch; genotyping;
 KW gene expression; ss.
 XX
 OS Synthetic.
 PN WO200107665-A2.
 PD 01-FEB-2001.
 XX
 PF 26-JUL-2000; 2000WO-US20476.
 PR 26-JUL-1999; 99US-0145695.
 PR 17-MAR-2000; 2000US-0190259.
 XX
 PA (CLIN-) CLINICAL MICRO SENSORS INC.
 XX
 PI Umek RM;
 DR WPI: 2001-159728/16.

Nucleic acids containing electron-transfer group, useful as labels in
 PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
 PT a single surface -
 PS Example 6; Page 128; 159pp; English.

The present invention relates to a composition comprising two nucleic
 CC acids each containing an electron-transfer group (ETM) having
 CC different redox potentials. The invention is used for electronic
 CC detection of nucleic acids, especially of substitutions (mismatches)
 CC and single-nucleotide polymorphisms, e.g. for genotyping,
 CC monitoring gene expression.

Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;

Query Match 12.7%; Score 264.6; DB 22; Length 936;
 Best Local Similarity 0.8%; Pred. No. 2.3e-31;
 Matches 6; Conservative 606; Mismatches 175; Indels 0; Gaps 0;

QY 115 ATATAGCAATTTGTTGAAAGGTTTATATATAGCTAAATTTGATTCATTTTC 174
 DB 2 WWWWWW 61
 QY 175 ATATATCTGAACAAGATGATGTAATTTGATTCATTTAGACATGATGAAAAAGT 234
 DB 62 WWWWWW 121
 QY 235 TAACGATTAGTCTTTTAAATTTCAATATAATTTTGGCCAAACTTTTGGCA 294
 DB 122 WWWWWW 181
 QY 295 AATATCATGTGCAAAATATAATTTGAAAAACAACAATATCAAACTTTTGGCAAC 354
 DB 182 WWWWWW 241


```

QY 355 AACTTTACAAAATCCATTTTCAGAAAAAATTTACATTACTGGCAATCAATT 414
Db 242 .....
QY 415 GTGTATGAAAAATTTAAATTCCTTACCTATATGAACTCAAGTGTAAATTT 474
Db 302 .....
QY 475 AGAAAAAGGAAAAATTTAAATTCGCAATTTATCGCAATCAATTTGTATGAAAAC 534
Db 362 .....
QY 535 TTAATATTTTATTTAAATATATGAAATTCAGAGTGTAAATTTAGAAAAAGGAAA 594
Db 422 .....
QY 595 AATTAAATGACCATTTCATTCAAAATGAGATTGTATGAAAAATTTAAATTTATTT 654
Db 482 .....
QY 655 CAATATATATGAACTGAAAGTGAACATTGAGAAAAAGGAAAAATTTAAATGATGA 714
Db 542 .....
QY 715 AATTTGTAAACATCAATTTGTGAAATCAGAAATTTAGCAAGTTAGACAAGAAAAAAC 774
Db 602 .....
QY 775 TGAATTTCTTATCTTTTCGGTACAAATTTGGGATCATAAGAAATTTACTGAATCCA 834
Db 662 .....
QY 835 TATCAAAACATATTTAATTAATTAACAAAATGAAATTAACCAAAAAAGAGACATGACGA 894
Db 722 .....
QY 895 TATTTGCG 901
Db 782 .....

```

RESULT 13

AAFS8255

ID AAF58255 standard; DNA; 938 BP.

AC AAF58255;

DT 24-APR-2001 (first entry)

DE Oligonucleotide D1876.

KW Electron-transfer group; ETM; mismatch; genotyping;

KM gene expression; ss.

XX Synthetic.

OS

PN WO200107665-A2.

PD 01-FEB-2001.

PE 26-JUL-2000; 2000MO-US20476.

PR 26-JUL-1999; 99US-0145695.

PR 17-MAR-2000; 2000US-0190259.

PA (CLIN-) CLINICAL MICRO SENSORS INC.

PI

XX time RM;

XX WPI; 2001-159728/16.

XX

XX Nucleic acids containing electron-transfer group, useful as labels in

```

PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface
XX
PS Example 6; Page 127; 159pp; English.
XX
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
SQ Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;

Query Match 12.7%; Score 264.6; DB 22; Length 938;
Best Local Similarity 0.8%; Pred. No. 2,3e-31;
Matches 6; Conservative 606; Mismatches 175; Indels 0; Gaps 0;

QY 115 ATATAGCAATTTAGTGAAGGCGTTTATATATGACTTAATTTGATTCATTTTC 174
Db 2 .....
QY 175 ATATATGAAAACAGATGTATGAAATTTGATTCATTTATGACACTGATGAAAACT 234
Db 62 .....
QY 235 TAACGATTTAGTCTTTTAAATTCATATATATTTTGCCCAAACTTTTGCAA 294
Db 122 .....
QY 295 AATATCCATTTGGAATTAATTTTGAAAACAAATATCAACCTTTTGGCAAC 354
Db 182 .....
QY 355 AACTTTACAAAATCCATTTTCAGAAAAAATTTAATTAATTTGCAATCAATTT 414
Db 242 .....
QY 415 GTGTATGAAAAATTTAAATTCCTTTCACCTATATGAACTCAAGTGTAAATTT 474
Db 302 .....
QY 475 AGAAAAAGGAAAAATTTAAATTCGCAATTTATCGCAATCAATTTGTATGAAAAC 534
Db 362 .....
QY 535 TTAATATTTTATTTAATATATGAAATTCAGAGTGTAAATTTAGAAAAAGGAAA 594
Db 422 .....
QY 595 AATTAAATGACCATTTCATTCAAAATGAGATTGTATGAAAAATTTAAATTTATTT 654
Db 482 .....
QY 655 CAATATATATGAACTGAAAGTGAACATTGAGAAAAAGGAAAAATTTAAATGATGA 714
Db 542 .....
QY 715 AATTTGTAAACATCAATTTGTGAAATCAGAAATTTAGCAAGTTAGACAAGAAAAAAC 774
Db 602 .....
QY 775 TGAATTTCTTATCTTTTCGGTACAAATTTGGGATCATAAGAAATTTACTGAATCCA 834
Db 662 .....
QY 835 TATCAAAACATATTTAATTAATTAACAAAATGAAATTAACCAAAAAAGAGACATGACGA 894
Db 722 .....
QY 895 TATTTGCG 901

```


XX	
DR	WPI; 1999-243728/20.
XX	

New apoptosis-resistant virus-sensitive cell

Example 2; Page 41-45; 51pp; English.

CC The present invention describes an apoptosis-resistant virus-sensitive
CC cell line into which an apoptosis resistance gene has been introduced.
CC The recombinant viruses generated are capable of expressing apoptosis-
CC associated genes. These can then be used in a variety of diseases for
CC which the induction of apoptosis by gene transfer, or where the
CC inhibition of harmful apoptosis, is therapeutic. The recombinant viruses
CC are useful as vectors for gene therapy which can be applied to cancer
CC therapy for destroying cancer cells selectively, the treatment of
CC autoimmune diseases and graft rejection reaction, and apoptosis induction
CC therapy for inflammatory cells in inflammatory diseases. Prior arts have
CC encountered the problem where if an adenovirus vector capable of
CC expressing an apoptosis-associated gene is introduced into animal cells,
CC the cells producing the virus will be destroyed because the period of
CC time required to induce cell death by apoptosis is shorter than that
CC required to replicate and produce the virus, resulting in failure to
CC obtain a recombinant virus having the integrated apoptosis-associated
CC gene. In this invention an apoptosis-resistant 293 cell line (having an
CC apoptosis resistant gene introduced) is established and overcomes the
CC problem. The present sequence represents the base sequence of the
CC plasmid pRX-Bcl-1, which contains the human Bcl-xL gene, and
CC is used in an example from the present invention.

Sequence 7372 BP; 2353 A; 1749 C; 1649 G; 1621 T; 0 other;

Query Match	6.3%	Score 131;	DB 20;	Length 7372;
Best Local Similarity	49.3%;	Pred. No. 1.6e-11;		
Matches 341;	Conservative 0;	Mismatches 350;	Indels 0;	Gaps 0

OY	3322	AAAAAACAACAAATATCAAAACCTTTTGGCAACAACCTTTTACAAAATTCATTTTCAGAA	381
Db	4469	aa	45289
OY	382	AAAAAAATTTACATTTAACTTGGCAAAATCAAAATTTGTATGAAAAAATTTTAAATTTTCCTT	441
Db	4529	aa	45868
OY	442	CACCTATATTTGAACTCAGAGTGTTTAAATTTAGAAAAAGGAAAAATAAAAATGACC	501
Db	4589	aa	4648
OY	502	ATTTCAATCGCAATCAAAATGTGTATGAAAAACTTAAATTTTATTTATATATATGA	561
Db	4649	aa	4708
OY	562	AATTCAAAGTGTTAAATTTAGAAAAAGGAAAAAATTTAAATGACCATTTCATCAAAAT	621
Db	4709	aa	4768
OY	622	CAGATTGTATGAAAAATTTAAATTTTATTTCAAAATTTAAATTCAAATCAGAACTGCA	681
Db	4769	aa	4828
OY	682	ACATTTGAAAAGAGGAAAAATTTAAATATATGAAAATTTGTAAACATCAATTTGTGAA	741
Db	4829	aa	4888
OY	742	TCAGAAATTTGGAAGTTAGACAGCAAGAAAAAAATCGATTTGTCTTACTTTTCGGTTACA	801
Db	4889	aa	4948
OY	802	ATTTGGGATCATTAAGAAATTAAGTGAATTCATCAAAACCTTTATTAATTTACAAA	861
Db	4949	aa	5008
OY	862	ATGAAATTAACCAAAAAAGAAAGACATGACATATTTTCGTAAAGACATCATCTGATT	921

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Db      5009  aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 5066
Qy      922  ATAAAGACATGGCATATTGACAATTGGAACCAAAAACATTCATAAATCACAAAAAT 981
Db      5069  aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 5126
Qy      982  GGTATACACATCTCAAAGACATGGAAGAAT 1012
Db      5129  aaaaaaaaaaaaaaaaaaaaaaaaaagaat 5159
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Search completed: February 23, 2002, 08:39:10
Job time: 7567 sec
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Sat Feb 23 11:04:38 2002

us-09-636-826-1.rng

Page 14

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 23, 2002, 05:19:02 ; Search time 53.82 Seconds
(without alignments)
8794.854 Million cell updates/sec

Title: US-09-636-826-1

Perfect score: 2090

Sequence: 1 GATATCACACATTCGTGCAT.....TCGCTTTCTGGTGTGCT 2090

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 351203 seqs, 11328999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents_NA.*

1: /cgn2_6/ptodata/2/ina/5A.COMB.seq.*

2: /cgn2_6/ptodata/2/ina/5B.COMB.seq.*

3: /cgn2_6/ptodata/2/ina/6A.COMB.seq.*

4: /cgn2_6/ptodata/2/ina/6B.COMB.seq.*

5: /cgn2_6/ptodata/2/ina/PTCUS.COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	4.6	19124	2	US-08-487-826B-13
2	75.2	3.6	615	4	US-08-998-416-186
3	74	3.5	5852	1	US-07-867-106-2
4	73.6	3.5	837	4	US-08-988-416-288
5	72.6	3.5	665	2	US-08-883-795A-36
6	70.8	3.4	658	4	US-08-998-416-595
7	69.4	3.3	7218	1	US-08-232-463-14
8	69.4	3.3	19124	2	US-08-487-826B-13
9	69.2	3.3	636	4	US-08-998-416-1137
10	68.6	3.3	8920	2	US-09-056-075-1
11	68.4	3.3	8920	2	US-08-446-855A-1
12	68.4	3.3	8920	4	US-09-150-741-1
13	66	3.2	1689	1	US-07-991-867B-41
14	66	3.2	1689	2	US-08-544-332-41
15	66	3.2	3095	6	5231168-1
16	66	3.2	8457	1	US-07-991-867B-1
17	66	3.2	8457	2	US-08-544-332-1
18	65.6	3.1	4818	1	US-08-817-926-27
19	65	3.1	1511	1	US-07-991-867B-8
20	65	3.1	1511	2	US-08-107-755A-8
21	65	3.1	1511	2	US-08-544-332-8
22	65	3.1	2447	2	US-09-014-969-14
23	64.8	3.1	51952	2	US-08-947-823-1
24	64.6	3.1	3933	2	US-08-731-722-3
25	64.6	3.1	3933	2	US-08-731-722-3
26	64.4	3.1	51952	2	US-08-947-823-1
27	63.6	3.0	2539	3	US-08-749-522-3

28	63.4	3.0	1431	4	US-09-316-083-2	Sequence 2, Appl
29	63.2	3.0	1511	1	US-07-991-867B-8	Sequence 8, Appl
30	63.2	3.0	1511	1	US-08-107-755A-8	Sequence 8, Appl
31	63.2	3.0	1511	2	US-08-544-332-8	Sequence 8, Appl
32	62.4	3.0	7218	1	US-08-232-463-14	Sequence 14, Appl
33	62.2	3.0	240	1	US-08-628-417-6	Sequence 6, Appl
34	61.6	2.9	2030	2	US-08-705-937-7	Sequence 7, Appl
35	60.8	2.9	6243	2	US-09-056-075-1	Sequence 6, Appl
36	60.6	2.9	8247	2	US-08-998-416-535	Sequence 535, App
37	60.4	2.9	665	2	US-08-883-795A-36	Sequence 36, Appl
38	60.4	2.9	782	4	US-09-007-119-15	Sequence 15, Appl
39	60.2	2.9	732	4	US-08-998-416-1036	Sequence 1036, Ap
40	60.2	2.9	4140	3	US-08-894-731-2	Sequence 1, Appl
41	59.8	2.9	6152	4	US-08-973-462-1	Sequence 1, Appl
42	59.6	2.9	1676	4	US-09-009-443-1	Sequence 10, Appl
43	59.4	2.8	5181	1	US-08-257-073-10	Sequence 1, Appl
44	59.4	2.8	6768	1	US-08-107-755A-1	Sequence 1, Appl
45	59	2.8	1230	4	US-09-140-466-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-08-487-826B-13

Sequence 13, Application US/08487826B

Patent No. 5993827

GENERAL INFORMATION:

APPLICANT: Sim, Kim L.

APPLICANT: Chitnis, Chetan

APPLICANT: Miller, Louis H.

APPLICANT: Peterson, David S.

APPLICANT: Su, Xin-zhaun

APPLICANT: Wellens, Thomas E.

TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX

TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe Martens Olson & Bear

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STATE: California

COUNTRY: US

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,826B

FILING DATE: 10-SEP-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Israelson, Ned

REGISTRATION NUMBER: 29,655

REFERENCE/DOCKET NUMBER: NIH121.001CPI

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550

TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 19124 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-487-826B-13

Query Match

4.6%; Score 97; DB 2; Length 19124;


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QY 510 CCAATTCATTTGCTATGAAACAACTTAAATTTTAAATTAATTAATGCAATTCAA 563
Db 2192 ATTAATTTAAATTTGCATGCCCAAACTGATTAATTTTGATATATATATCCAAATTTTATTA 2133
QY 570 GTGTTAAATTTAGAAAAAGGAGAAAAATTTAAATGACCAATTCATTCATAAATCAGATTTGT 629
Db 2132 ATTAAGCTATATTTGATAGTAGAATAATTAATTTTAATTTTATAAAAAAAATCATAAAAAA 2073
QY 630 GTATCAAAAAATTTAAATTTTATTTTCAAAATATATATTGAAACTCGAAAGTGAACATTTAG 689
Db 2072 ACCAAGTAATTAATTAATTTAATGAAGGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2013
QY 690 AAAAGAGCAAAAAATTTAAATATGATGAAATTTGTAAACATCAATTTGCAATTCGAATTT 749
Db 2012 CAAAGTAAAAAATAAAAAAAAAAAAAAAAAAGAAATGAAAAAAGGTGTTAACTACATCTT 1953
QY 750 TAGAAGTTAGA-----CAAGGAAAAAATAACGTAATTTGCTTATTTACTTTTCGGTTCAATTT 804
Db 1952 AGTTTTTATAGTTTGTTCATATTTTAAATAATCACTTTTATTTTAATTTAGATTTTAAATTT 1893
QY 805 TTGGATCATATAAATAATTTACTGAATCCATATCAAAAACTTTATTAATTTACAAAAAATG 864
Db 1892 ATGGAATCTAATTAATAAAAAAAATTTTAAATTTTAAAAAAGAAAAAAGAAAAAATAAAAAA 1833
QY 865 AATAAAACCAAAAAAAGACAGACATCGCATATTTGCTAAGAGACATCATCTGATTTA 924
Db 1832 AGTGAATTTATTTAATAATTTTAAATATTTATTCATCTTTAATTAATTAAGTATATATTCGAT 1773
QY 925 AAGAGACATGCGCATATTTAGAAATTTGAGAAACAAA 958
Db 1772 AGGCAATTTATTTTATATCTATCTAATAAAAAA 1739

RESULT 4
US-08-998-416-288/c
; Sequence 288, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippesen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Redischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPYI
; TITLE OF INVENTION: AND USUS THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/GC91976
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: 919-541-8587
 TELEFAX: 919-541-8689
 INFORMATION FOR SEQ ID NO: 288:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 837 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: PAG1241RP
 US-08-998-416-288

Query Match 3.5%; Score 73.6; DB 4; Length 837;
 Best Local Similarity 47.8%; Pred. No. 3e-05;
 Matches 282; Conservative 0; Mismatches 299; Indels 9; Gaps 2;

162 TTGATTCATTTTCATATATCTGAAACAGGTATGTGAAATTTGATTCATTATGACA 221
 11
 Db 597 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 538
 11
 Oy 222 CTGATGAAAGTTAAGCATTTAGTCTTTTAAATTCATTAATTAATTTTCC 281
 11
 Db 537 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 478
 11
 Oy 282 AAAACCTTTGCAAAATATCCATGTTGCAAAATTAATTTGAAAAACAAATATCA 341
 11
 Db 477 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 418
 11
 Oy 342 CCTTTTGCAGAACCTTTTCCAAAATCCATTTTCAGAAAAAAAATTTTCACTACT- 400
 11
 Db 417 TTTATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATC 358
 11
 Oy 401 -----TGCAGAAATCAATTTGTATGAAAAATTTAAATTTCCCTTACCTTAATG 453
 11
 Db 357 TTTATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATG 298
 11
 Oy 454 AAACCTCAAGTGTAAATTTTGAAAAAGAGAAAAATTAATAAGACATTTCATGCGAA 513
 11
 Db 297 AATAATCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 238
 11
 Oy 514 ATCAATATGCTGATGAAAAATTTAAATTTTAAATTTAAATTTGAAATTCAGAAATG 573
 11
 Db 237 ATTTAAATTTGACATGACATAATTAATTAATTAATTAATTAATTAATTAATTA 178
 11
 Oy 574 TAAATTTAGAAAAGAGAGA-AAATTAATGACATTTCATTCAAAATCGAATTTGTA 632
 11
 Db 177 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 118
 11
 Oy 633 TGAATAATTTAAATTTTATTTCAATATTAATTAATTAATTAATTAATTAATTA 692
 11
 Db 117 ATCAATAATTAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 58
 11
 Oy 693 AGCAGAAAAATTAATTAATTAATTTGTAACATCAATTTGTAAT 742
 11
 Db 57 ATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 8

RESULT 5
 US-08-883-795A-36
 Sequence 36, Application US/08883795A
 Patent No. 5985607
 GENERAL INFORMATION:
 APPLICANT: Delcive, Genevieve
 APPLICANT: Awang, Gregor
 TITLE OF INVENTION: Recombinant DNA Molecules and Expression
 TITLE OF INVENTION: Vectors for Tissue Plasmidogen Activator
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BERESKIN & PARR
 STREET: 40 King Street West
 CITY: Toronto

STATE: Ontario
 COUNTRY: Canada
 ZIP: M5H 3Y2
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/883,795A
 FILING DATE: 27-JUN-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Gravelle, Micheline
 REGISTRATION NUMBER: 40,261
 REFERENCE/DOCKET NUMBER: 7841-062
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 364-7311
 TELEFAX: (416) 361-1398
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 665 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: Rh 32
 US-08-883-795A-36

Query Match 3.5%; Score 72.6; DB 2; Length 665;
 Best Local Similarity 48.4%; Pred. No. 4.4e-05;
 Matches 290; Conservative 0; Mismatches 304; Indels 5; Gaps 3;

411 AATGTGTATGAAAAATTTAAATTTCTTTACCTATTAATTAATTAATTAATTAAT 470
 11
 Db 14 AATGTGTATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 73
 11
 Oy 471 ATTAGAAAAGAGAAAAATTAATAATGACATTTCATTCGAAATCAATTTGTATGAA 530
 11
 Db 74 ATT-AAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 131
 11
 Oy 531 AAACCTAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 590
 11
 Db 132 TAAATTAATTAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 191
 11
 Oy 591 GAAAAATTAATAATGACATTTCATTCMAAATGATTTGTATGAAAAATTTAAATTT 650
 11
 Db 192 TAAATTAATTTTAAATTAATTAATAATTTAATTAATTAATTAATTAATTAATTA 251
 11
 Oy 651 ATTCAATATTAATTTGAATCAAG--TGTGACATTTAGAAAAGAGAAAAATTA 708
 11
 Db 252 TAAATTAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 311
 11
 Oy 709 TGAATGAATTTGTAACATCAATTTGCAATTCAGAAATTTGAAGATTAGACAGAAA 768
 11
 Db 312 TAAATTAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 371
 11
 Oy 769 AAAAATGAATTTCTTATACCTTTGCTTACAAATTTGGATCATTAAGAAATTA 828
 11
 Db 372 TAAATTAATTTTAAATTAATAATGTTTAAATTAATTAATTAATTAATTAATTA 431
 11
 Oy 829 AATCCATTAATAAATCATTTATTAATTAACA-AAATGAATTAATAAACCMAAAGAA 887
 11
 Db 432 TAAATTAATTTTAAATTAATTAATTAATAAGATTTAAATTAATTAATTAATTA 491
 11
 Oy 888 ATGACATTTTGTGAAGAACATCAATGATTTATAAAGAAATGCGCATTTAGAA 947
 11
 Db 492 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 551

QY 948 TGAGAAACAAAACACTATTCACAAAATGAGATACACATACAGAACATGCA 1006
DB 552 TCAATATTTTATTAATAGTTAAAGACGAGAGAAAAATTAAAGACAGAGTTATTCGA 610

RESULT 6

US-08-998-416-595/C

Sequence 595, Application US/08998416
Patent No. 6239264

GENERAL INFORMATION:

APPLICANT: Philippson, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Redischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPITII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwells Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/998.416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689

INFORMATION FOR SEQ ID NO: 595:

SEQUENCE CHARACTERISTICS:
LENGTH: 658 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE: PAG1408RP
ORGANISM: PAG1408RP
US-08-998-416-595

Query Match 3.48; Score 70.8; DB 4; Length 658;

Best Local Similarity 47.8%; Pred. No. 9.2e-05;

Matches 236; Conservative 0; Mismatches 257; Indels 1; Gaps 1;

QY 477 AAAAGGAGAAAATTAATAATGACCAATTCATGCGAAATCAAAATGTTGATGAGAAAACTT 536
DB 653 AAAATTAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 594
QY 537 AAA-ATTTTAAATTAATTAATGAATCAAGTCTTAATTAATTAAGAAAAGAGAGAAA 595
DB 593 AAAATTAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 534
QY 596 ATTAATGACCATTCATTCATCAAAATCAGATTTGTGATGAGAAAATTAATTTTATTTTC 655
DB 533 AGAAATAGCATATATATATATATGTCACAAAATCAATCTATATATGAATTAAGTACCAAT 474

QY 656 AATATATATGAACCTCAAGGTGAGACATTTGAAAAGAGAGAAAAATTAATGATGAA 715
DB 473 AATATACTATCTAT 414
QY 716 AATTTGTAAGACATCAATTTGTGAATCAGAAATTTGAACTTGACAGAGAAAAAACT 775
DB 413 AAAATACATTAATAATAAGGTATTAATTAATAATAATAATAATAATAATAATAATA 354
QY 776 GAATGCTTATACCTTTTCGTTACATTTTGGATCATTAAGAAATTCGAATTCAT 835
DB 353 AAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 294
QY 836 ATCAAAACATTAATAATTCACAAAATGATTAACCAAAAAGAGAGACATGACAT 895
DB 293 AATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 234
QY 896 ATTTGTAAGACATCAATCTGATTAATAAGACATGCGCATTTAGATGAGAAAC 955
DB 233 AATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 174
QY 956 AAAAATCTATTCOA 969
DB 173 CAAAGCATCTMAAA 160

RESULT 7

US-08-232-463-14/C

Sequence 14, Application US/08232463
Patent No. 5670367

GENERAL INFORMATION:

APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 diagonal Road, Suite 500
CITY: Alexandria
STATE: VA

COUNTRY: USA

ZIP: 22313-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 30472/114 IMMU

TELEPHONE: (703)836-9300

TELEFAX: (703)683-4109

TELEX: 899149

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ9pt-F15

US-08-232-463-14

```
Query Match      3.3%; Score 69.4; DB 1; Length 7218;
Best Local Similarity 8.4%; Pred. No. 0.00021;
Matches 37; Conservative 230; Mismatches 176; Indels 0; Gaps 0;
```

```

Oy 569 AGTGTAAATTTTGGAAAGGAGAAAAATTTAAATGACCATTTTCATTCGAAATCGATG 628
Db 1513 AGTTCAAAAACCGCATGTAGSCATCAGCTAATTACTATCTATGCAAGTAAAG 1454
Oy 629 TGTATGAAAATTTAAATTTTATTTCGAAATATATGAAACTCAAAGTGGACATTTA 688
Db 1453 AGATAGAGAAGATTTGTGTCRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1394
Oy 689 GAAAGGAGAAAATTTAAATGATGAAAATTTTAAACATCAATTGTGGAATCAGAT 748
Db 1393 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1334
Oy 749 TTAGAGTTAGACAAGAAAAAAACTGAATTGCTTATACTTTCGTTACATTTTG 808
Db 1333 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1274
Oy 809 GATCATAAAGAAATTTACTGGAATTCATATCAAAAACATATTATAAATACAAAAAGATA 868
Db 1273 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1214
Oy 869 AAACCAAAAAAGAGAACATGACGATATTCTTAAGAACATCAATGATTATAAAG 928
Db 1213 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1154
Oy 929 AACATGGCATATTAGATTGAGAAACAAAAAACTATTCAAATTCACAAAAATGCATAC 988
Db 1153 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1094
Oy 989 AACATCAAAAGAACATGAAGAA 1011
Db 1093 RRRRRRRRRRRRRRRRRRRRRR 1071

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1      RESULT      8
2      US-08-487-826B-13/C
3      ; Sequence 13, Application US/08487826B
4      ; Patent No. 5993827
5      ;
6      GENERAL INFORMATION:
7      ;
8      APPLICANT:  Sim, Kim L.
9      ;
10     APPLICANT:  Chitnis, Chetan
11     ;
12     APPLICANT:  Miller, Louis H.
13     ;
14     APPLICANT:  Peterson, David S.
15     ;
16     APPLICANT:  Su, Xin-zhaun
17     ;
18     APPLICANT:  Wellens, Thomas E.
19     ;
20     TITLE OF INVENTION:  BINDING DOMAINS FROM PLASMODIUM VIVAX
21     ;
22     TITLE OF INVENTION:  AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
23     ;
24     NUMBER OF SEQUENCES:  45
25     ;
26     CORRESPONDENCE ADDRESS:
27     ;
28     ADDRESSEE:  Knobbe Martens Olson & Bear
29     ;
30     STREET:  620 Newport Center Drive  16th Floor
31     ;
32     CITY:  Newport Beach
33     ;
34     STATE:  California
35     ;
36     COUNTRY:  US
37     ;
38     ZIP:  92660
39     ;
40     COMPUTER READABLE FORM:
41     ;
42     MEDIUM TYPE:  Floppy disk
43     ;
44     COMPUTER:  IBM PC compatible
45     ;
46     OPERATING SYSTEM:  PC-DOS/MS-DOS
47     ;
48     SOFTWARE:  Patentin Release #1.0, Version #1.25
49     ;
50     CURRENT APPLICATION DATA:
51     ;
52     APPLICATION NUMBER:  US/08/487,826B
53     ;
54     FILING DATE:  10-SEP-1993
55     ;
56     CLASSIFICATION:  435
57     ;
58     ATTORNEY/AGENT INFORMATION:
59     ;
60     NAME:  Israelsen, Ned
61     ;
62     REGISTRATION NUMBER:  29,655
63     ;

```

REFERENCE/DOCKET NUMBER: NIH121.001CPI
TELECOMMUNICATION INFORMATION:
6510 22 9550

TELEPHONE: (619) 235-8550

TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs

LENGTH: 19124 base p
TYPE: nucleic acid

TYPE: nucleic acid
STRANDNESS: single

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

US-08-487-826B-13

Query Match	3.3%;	Score 69.4;	DB 2;	Length 19124;
Best Local Similarity	46.1%;	Pred. No. 0.00023;		
Matches 350;	Conservative	0;	Mismatches 396;	Indels 13; Gaps 3.

OY	54	TTCCTTAAATCCTTCAAGATTATTCACACTTGTCGATTAATGAATGAGTGAATAAATGGA	113
Db	18352	TTTTTTTTTTTTTTTTTTTTTTTGTGATAGTAGTGAGTAATCCTTAATGCTTTTTTGTTGAT	18293
OY	114	GATMAATAGAATTAGTGGAAAAGGTGTTATATATAATAGACTTAATTTGATTCATTTT	173
Db	18292	AAAAGATTAAGAAATTAATAAAGCAATAAAGTAAATTAATAAATAAGAAATTTAGTTATAT	18233
OY	174	CATATATCGAAAACAGTAGTATGAATTTATTCATTCTTATGACACTGATGAAAAAG	233
Db	18232	TATATAAATPACAGAAATATATTTGTATATATTAATTAATTTTATTTAATAGGAACCTAT	18173
OY	234	TTTAACGAT-----TAGTCTTTTCTTTTTPAAAATTTCCAATATATAATTTTGGCCAAACT	287
Db	18172	ATATATATTGATTTATTAATAATTTTTTATATAGAGATTATATATTTTTTTTCCGTGGANT	18113
OY	288	TTTGC AAAATATCCATGTTGCGAAATVAAATTTTGAAAACAAAACAATATCAACCCTTT	347
Db	18112	ATTGAGATTAGAGTAACA AAATTAACACATATATATAAACACATATATAATACAT	18053
OY	348	TGCGAACACTTTTACAAAATTCATTTTCAGAAAAAAAATTTTACATT-----ACGT	401
Db	18052	TTAAATATATATTAATAAAATVTCCAAATTAATTAATTAATTAATTAATCTGAAAAAATG	17993
OY	402	GCGAAATCAATGCTATAGAAAATTTTAAATTTCCCTTCACCTAATTAATGAACTCA	461
Db	17992	AAAAATCGAAATAGAGAGATATATATTTTGGAAAAAGGAATATATATATATATATA	17933
OY	462	AGTCTTAAATTTTGAAGAAAGAGAAAAATTA AAAATGACATTTTCATGCGAAATCAAT	521
Db	17932	TATATATATTAAGCAAAAATGTACGAAAAAGAAAACA AATTAACATATATCATTAAT	17873
OY	522	GCTATCAAAACCTTAAATTTTATTTTAATTAATTAATTTGAAATTCAAAGTGTTAAATTT	581
Db	17872	ATTATATCAAAATATAGATACAAATTAATTAATACAAAAAATAAATAATACATATATATVAAA	17813
OY	582	AGAAACGCAAAAATTAATAATGACCATTCCTCAAAATCAGATGTGTATGAAAAAT	641
Db	17812	TATTTATAAAAAATTTACCAATTAAGAAAAGAAAAAAAATTCATGTTGCCAATTTVTTA	17753
OY	642	TAAATTTTATTTCAATATAATTAATGAACTCAAACTGTGAACATTTTGAAAAAGAGAAA	701
Db	17752	AAATATATATATATGATTTATATAACAAAAACAATTTTTTACAAATATVACCAAAAAACATA	17693
OY	702	ATTAAATGATGAAATTTGTAAACATCAATTTCTGAA-ATCGAATTTTGAAGTTAAG	760
Db	17692	AATTAATTAATTAATTAATAAATAAACAATATCAAAATATATCAAAAATATATATAGACA	17633
OY	761	CAAGSAAAAAAAACTGAATGCTCTATACTTTGCGTTA	799
Db	17632	CACACAAAAAAGTATTTATTTTATTTTATTTGATATTCATATA	17594

Query Match	3.3%	Score 69.2	DB 4	Length 636
Best Local Similarity	48.1%	Pred. No. 0.00018		
Matches 299	Conservative	0	Mismatches 308	Indels 15
			Gaps	3
QY	ATCCATTTTCAGAAAAAAATTTTCATTACTGCGAATCAATGTTGATGAAAT	427		
Db				
620	AATCATATCTTTATATATTTTATTATTATTAATTAATGATAAATTTTAATTAAT	561		
QY	428 TTAAATTTTCCTTCACCTATATATGAACTCAAAGTGTAAATTTGAGAAAAGAGA	487		
Db				
560	AATTAATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	501		
QY	488 AATAAAAATGACATTTTCATGCGAATCAATGTTGATGAAAACTTAAATTTTAT	547		
Db				
500	AATTAATTAATTAAGAAATTAAGCTTAATTTTATTAATTTCTTTTAAAAAGATT	441		
QY	548 T--TAAATTAATTAATTAATTAATTAATTTGAAAAAGCAGAAAAATTAATTAATGA	605		
Db				
440	AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT	381		

OY		606	CCATTCATTCAAAACGAGTGGGTATGAAAATTTAAATTTTTTAATTCACAATATAAT	665
Dp		380	ACATATATTTAATTAATTTAAATCTTTATTAATATAAAAAATATATATTAATTAATTAACAAAT	321
OY		666	GA-AACTCAAGTGTAACATTTTAGAAAAGCAGAAAATTAATAATGATGAATTTGTAA	724
Dp		320	AATTAATTAATATTAATTAATTTGATTAATATCATTTTAATTAATTTTAACAAAATATATAT	261
OY		725	AACATCAATTTTGGAATCAGAAATTTAGAGTTAGCACAGGAAAAAACCTGAATTTGCT	784
Dp		260	ATCTAATTAATTTTAAATTAATTAACATTTTAAATTTGAAACATGACTAAATAGTATTCATAT	201
OY		785	TATACCTTTTCGGTTTCAAAATTTGGAGTCATPAAGAAATTAATCTGAATTCATATCAAAAC	844
Dp		200	TAAATATTTATTTTATTATTAATTTATTAATATTTAATA-----TGATGAATTTAG	153
OY		845	TATTTAATAATTCAAAAAATGAAATAAACCAAAAAAGAAGACATGACGATATTTTGTAA	904
Dp		152	TAAATTAATTAATTAATTTATTAATTAAGATTAATTAATCAAAATTAATTAATTAATAA	93
OY		905	AGAACATCATCTCGATTTTAAGAGACATGCGCATTTTAATTTGAAACAAAAAACTA	964
Dp		92	TGATATATATAGTTAAATTAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	33
OY		965	TTCAAATCACAAAATATGATA	986
Dp		32	TCTTTAATTAATTAATTAATA	11
 RESULT 10 US-09-056-075-1 Sequence 1, Application US/09056075 Patent No. 5953368 GENERAL INFORMATION: APPLICANT: Johnson, Eric A. APPLICANT: Bradshaw, Marile APPLICANT: Rood, Julian TITLE OF INVENTION: Expression System for Clostridium NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSEE: Quarles & Brady STREET: 1 South Pinckney Street CITY: Madison STATE: WI COUNTRY: US ZIP: 53701-2113 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/056,075 FILING DATE: CLASSIFICATION: ATTORNEY/AGENT INFORMATION: NAME: Seay, Nicholas J. REGISTRATION NUMBER: 27386 REFERENCE/DOCKET NUMBER: 960296,95238 TELECOMMUNICATION INFORMATION: TELEPHONE: 608-251-9166 TELEFAX: 608-251-9100 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 6243 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) FEATURE: NAME/KEY: misc_feature LOCATION: 3770..4013				

```

; OTHER INFORMATION: /note= "RP4 origin of DNA transfer (orit) from
; OTHER INFORMATION: plasmid RP4"
US-09-056-075-1

```

Query Match	3.3%	Score 68.6;	DB 2;	Length 6243;
Best Local Similarity	47.0%;	Pred. No. 0.00029;		
Matches 256;	Conservative	0;	Mismatches 279;	Indels 10;
				Gaps 1;

QY	392	ACATTACCTTCGGAATCAATATGTCATGAGAAATTAATAATTTCTTCACCTTAAT	451
Db	860	ACTTTTAATTAATAAATGAAGACTTTAAACTGCTTTTATATTAATTAAATGAAGT	919
QY	452	TGAACCTCAAGTGTAAATTTGAAAAGAGGAAAAATAAAAATGACATTTCATCG	511
Db	920	TTTATCAAAAAAATTTCCAAATATCCACACTTAAGCCACAACACGCCCTATTAATCCC	979
QY	512	AAATCAAAATTTGTATGAAAACCTTAATAATTTTATTAATATTAATTGAAATTCAAAGT	571
Db	980	GCTTTAAATCCCATTTTGAGACACATGTAATTAATCTTTAGGCCCTAGTATAGTATATT	103
QY	572	GTTAAATTTTGAAAAGAGAAAAATTAATAATGACATTTCAATCAAAATCAGATTGTG	631
Db	1040	TTTTCATTTCAATGATCCGACGCAAAAAATTAAGGSGCATATATAAAGTTCCCTCGAA	109
QY	632	ATGAAAAATTTTAAATTTTATTTTCAA-----ATATTAATTGAAAGCTCAAAAGTGTGA	681
Db	1100	CTACTAATAGTAAAAAATTAATCTTTACACACTCCCAAAAAAAGACAGAGTCAAGTA	115
QY	682	ACATTACAAAAGGAGAAAAATTTAAATGATGAAAATTTGTAAACATCAATTTGTGAA	741
Db	1160	CCCTTAATTAACAGGCTAAAAAATGAGGGTAAAAAATAAAAAATTAATAAAAAA	121
QY	742	TCAGATTTAGAGTTAGACAGAAGAAAAAAATCAAGATTGCTATCTTTGCGTTACA	801
Db	1220	TAAAAAATTAATAAATTAATAAATTAATAAATTAATAAATTAATAAATTAATAAATAA	127
QY	802	ATTTTGGGATCATAAAGAATTTACTGAATTCATATCAAAAACTATTATAATTCACAAA	861
Db	1280	AAAAATTAATAAATTAATAAATTAATAAATTAATAAATTAATAAATTAATAAATAA	133
QY	862	ATGAATTAATACCAAAAAAGAGAACATGACGATATTTTCGTAAGAAGACATCATCTGATT	922
Db	1340	ATTAATAAATAATATTAATAAATTAATAAATTAATAAATTAATAAATTAATAAATAAT	139
QY	922	ATTAAT 926	
Db	1400	AAAAA 1404	

RESULT 11
US-08-446-855A-1
; Sequence 1, Application US/08446855A

```

: GENERAL INFORMATION:
:
: APPLICANT: Stewart, Thomas S
:
: APPLICANT: Flores, Maria V
:
: APPLICANT: O'Sullivan, William J
:
: TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
:
: TITLE OF INVENTION: phosphate synthetase II
:

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ADDRESS: Nixon & Vanderyhe PC
STREET: 1100 No. 584573th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:

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3      COMPUTER READABLE FORM:
4      DATE: 220204 1117
5
6      MEDIUM TYPE: Floppy disk
7
8      COMPUTER: IBM PC compatible
9
10     OPERATING SYSTEM: PC-DOS/MS-DOS
11
12     SOFTWARE: PatentIn Release #1.24
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1: CURRENT APPLICATION DATA:
2: APPLICATION NUMBER: US/08/446,855A
3: FILING DATE: 06-Jul-1995
4: CLASSIFICATION: 435
5: ATTORNEY/AGENT INFORMATION:
6: NAME: Milchard, Leonard C
7: REGISTRATION NUMBER: 29,009
8: REFERENCE/DOCKET NUMBER: 47-80
9: TELECOMMUNICATION INFORMATION:
10: TELEPHONE: 703-816-4000
11: TELEFAX: 703-816-4100
12: INFORMATION FOR SEQ. ID NO.: 1:
13: SEQUENCE CHARACTERISTICS:
14: LENGTH: 8920 base pairs
15: TYPE: nucleic acid
16: STRANDEDNESS: single
17: TOPOLOGY: linear
18: MOLECULE TYPE: genomic
19:
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Query Match	3.3%;	Score 68.4;	DB 2;	Length 8920;
Best Local Similarity	44.8%;	Pred No. 0.00032;		
Matches 304;	Conservative 0;	Mismatches 371;	Indels 3;	Gaps 1;

OY	323	AAACCAAAACAAATATCAAACTTTTGGCAACACTTTTCAAAAATCCATTTTCGAAA	382
Db	114	AACACAGAAAAGACATAAATCTTTAAAGCTTTGACGAAATAATTAATAAATAA	173
OY	383	AAAAAATTACATTAACTTGGGAATCAAAATTTGTATGAAAATAATTTAAATTCCTTC	442
Db	174	TAAAAAGATAAATAATTTATTTGATTTGATCTGTATATATATATGATTTATCATATTA	233
OY	443	ACCTATATTGAACCTCAAACTGTAAATTTAGAAAAAGGAATAATTAATAATGACA	502
Db	234	TAACTATATAAAAACCTTTTTTTTTTTTTTTCTTTATATTTATTAACAATACATT	293
OY	503	TTTCATCGGAATCAAAATTTGTATGAAAACCTTAAATTTATTTAAATTAATGAA	562
Db	294	TAAATTTATTTATGTTG	353
OY	563	ATTCAAAGTCT---TAAATTTACAAAAGGAGAAAATTTAAATGACCATTTCAATCAA	619
Db	354	TGTTCAATTTGTTTAAATAATTTACTGGAATATPAAACCTTATTAATATATTTTCATTAA	413
OY	620	ATCAGATTTGTATCAAAAATTTAAATTTTATTTTCAAAATTAATTAATGAACTCAAACTGT	679
Db	414	ATGAATACAAATTTATTAATTTTGTATGTCTACAAATTAATTAATTTTAACTCTTATA	473
OY	680	GAACTTTAGAAAAGGAGAAAATTTAAATGATGAAAATTTGTAAACATCATTTGTGA	738
Db	474	ATTAACAACATCTATATATTTTATACACAATATATATATCTCCCAATATTTGTTTCTAT	533
OY	740	AATCGAATTTTGAATTTAGACACAGGAAAAAAACCTGAATTTGTATACCTTTTCCGTTA	798
Db	534	AAATTTATTTATATTTATTTATTTATTAATTTATTCATTTATTTTCTTAGTTTA	598
OY	800	CAATTTGGGATCAATAAGAAATTTACTGAATTCATATCAAAAATTTAATTTCAA	858
Db	594	TAAATTAGTAATTTCTACTAATTTAAAAAATAAAAAAAAAAAAAAAAAAGAAAAA	655
OY	860	AAATGAATPAAACCAAAAAGAGAACACATCGCATTTTGTGAAGACATCTACTGA	919
Db	654	AAAAATTTTCAATGAAAATAATCACTTGTATATGTAAATTTATTAATTTTAAACATA	713
OY	920	TTATAAAGAACATCGCATATTTAGATTTGAGAAACAAAACCTATTCAAATCACAAA	977
Db	714	ATATTAATTTATAAAAAATAAAAAAGAAAAATGGGAAAAATAATATATATATATATA	773
OY	980	ATGATTAACACATCAAA 997	
Db	774	ATATATATATATATATAA 791	

RESULT 12
US-09-150-741-1
; Sequence 1, Application US/09150741
; Patent No. 6183996
; GENERAL INFORMATION:
; APPLICANT: Stewart et al.
; TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
; Patent No. 6183996
; TITLE OF INVENTION: Synthetase II
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/150,741
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: PL6380
; EARLIER FILING DATE: 1992-12-16
; EARLIER APPLICATION NUMBER: AU93/00617
; EARLIER FILING DATE: 1993-12-02
; EARLIER APPLICATION NUMBER: 08/446,855
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8920
; TYPE: DNA
; ORGANISM: Plasmodium falciparum
US-09-150-741-1

Query Match 3.3%; Score 68.4; DB 4; Length 8920;
Best Local Similarity 44.8%; Pred. No. 0.00032;
Matches 304; Conservative 0; Mismatches 371; Indels 3; Gaps 1;

QY 323 AAAACAAACAAATATCAAACTTTTTCGCAACAACTTTTCAAAAATTCCTTTGGA 382
DB 114 aacagagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaa 173
QY 383 AAAAATTTTCAATTAATCTCGAAATCAATTTGTATGAAATTTAAATTTCTTC 442
DB 174 taaaagataaaaataatattatattgatattgatattatattatattatattat 233
QY 443 ACCTATATGAAATCAAACTTTTAAATTTGAAAGAGAAATTTAAATTTCAACA 502
DB 234 taacataagataaaaacttttttttttttttttttttttttttttttttttttt 293
QY 503 TTTTCATGCAAAATCAATTTGTATGAAATTTTAAATTTTAAATTTTAAATTTGAA 562
DB 294 taagattattatataataataataataataataataataataataataataata 353
QY 563 ATTCAAAGTGT--TAAATTTGAAAGAGAGAAATTTAAATTTGACATTTTCATTC 619
DB 354 tggcatttgattataaataattacttgaataataaactattataattttccaatt 413
QY 620 ATCAGATTGTATGAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 679
DB 414 atgaatacaattataatttttgatgtcacacataacatgatttttaacttttata 473
QY 680 GAACATTTGAAAGAGAGAAATTTAAATTTGATGAAATTTTGAATTTGATTTGTA 739
DB 474 ataaaccatccatataattataacacataataaaccatccatattgtgttccat 533
QY 740 AATCAGAAATTTAGAAATTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 799
DB 534 aatttattataattattattattattattattattattattattattattattatt 593
QY 800 CAATTTGGAGATTAAGAAATTTACTGAATTCATATCAAAATTCATTTATTAATTA 859
DB 594 taaatagtaattctactaatttaaaaaaagaaagaaagaaagaaagaaagaaagaa 653
QY 860 AATGATATTAACCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 919
DB 654 aaaaattacataagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaa 713
QY 920 TTATTAAG 979

DB 714 atataatgtataaaaaaaagaaagaaagaaagaaagaaagaaagaaagaaagaa 773
QY 980 ATGATATACACATACAA 997
DB 774 atataatataataataa 791

RESULT 13
US-07-991-867B-41/c
; Sequence 41, Application US/07991867B
; Patent No. 5476781
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Hall, Richard L.
; APPLICANT: Grubel, Michael E.
; TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESS: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/991,867B
; FILING DATE: 12-DEC-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 92/14818
; FILING DATE: 12-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,685
; FILING DATE: 30-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/657,584
; FILING DATE: 19-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UFI14.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-991-867B-41

Query Match 3.2%; Score 66; DB 1; Length 1689;
Best Local Similarity 43.8%; Pred. No. 0.00072;
Matches 387; Conservative 0; Mismatches 490; Indels 7; Gaps 2;

QY 139 TGTATATTAATTAAGACTTAATTTGATTCATTTTATATATGAAAGAGATATGA 198
DB 943 TATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 884
QY 199 TGAATTTGATTCATTTATGACAGTGAATGAAAGAGAGAGAGAGAGAGAGAGAG 258
DB 883 CGTATTCAGATTAATTAATTAATTTCTGAAATTTAATTAATTAATTAATTAATTA 824
QY 259 AATTCATATTAATTTTTCGCCAAACCTTTTGCAGAAATTTCAATGTCGGAATTAAT 318

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      823 AAAAGTTATGATTAAGAGAGATATTAATTAATGAGAGTTAATTTTAAAGCA 764
      319 TTGAAAAACAAACATATCAACCTTTTTCGACACACTTTTACAAAATCCATTTC 378
      763 ATTAAAGAAACATATATAGCTATATCTTTTAAAGATTAATGAAACAGATGTT 704
      379 GAAAAAAATTTACATTAACCTGCGAATCAATTTGTATGAAAAATTTAAATTTCC 438
      703 AACGAAAAACAATTTATAGATGATGCAAAAAATATATTTTATCATATATATAT 644
      439 TTTCACCTATATGAAACCTCAAGCTTTAAATTTAGAAAGAGAAAAATTTAAATG 498
      643 TATGTCGATGAGCAATCTAATATATATATATGCGAGAAAAATATGATTTATAAC 554
      499 ACCATTTCATGCGAAATCAAAATTTGTATGAAAAATTTAAATTTTAAATATAT 558
      583 ATTAGGTGTTTAAACTATGAGACATTAATATCTTCATTTGCTTTTATGATCTTAA 524
      559 TGAATTTCAAAGTGTAAATTTAGAAAAAGAGAAAAATTTAAATGACATTTCATTC 618
      523 AATAAAGGAGATTTAGATTAATATATATATATATATATATTAAGAAAAACTTGT 464
      619 AATCAGATTTGCTATGAAAAATTTAAATTTTATTCAAATATATATGAAACTCAAG 678
      463 ATTTCCGAGTTTACAAAAATATATATTTCTGCAATCTTTTATGAAAGTTTAAAAA 404
      679 TGAACATTTAGAAAAAGAGAAAAATTTAAATGATGAAATTTGTAAACATCAATTT 738
      403 TGATATATTTAAAAATTAATAATTTACCAATCACTGATATATATATATATATAT 344
      739 AATCAGATTTAGATTAAGATTAAGAGAAAAATTTGCTATCTTATCTTTGCTT 798
      343 ATATCAATATTT---CGGTAAATATATATAGAACTTGTAAATATATTTAAATTCG 268
      799 ACAATTTTGGATCATTAAGAAATTTACTGAAATCCATATCAAAAATCTATTAATTA 858
      287 GAAAGATTTATATATTTTCAACCTTACTTATTTTGAAGAAATTCAGATTTAAATG 228
      859 AAATGATTAACCAAAAAAGAGAACATGACGATATTTTCCGTAAGAACATCATCTG 918
      227 ATTTTAATTT---GTTTATATTTTCTTATATATGAAATATCTAGCAAACTTTAA 171
      919 ATTATTAAGAACATGCGCATATTAATGATTAAGAGAAAAATTTTCAAAATCAACA 978
      170 GAGATTAATGATTAAGCAATATATATATTTTGAAGAAATTAATGTAAGAAAAAG 111
      979 AATGATTAACAACATACAAAGAACATGAAAGAAATCTTATTCACA 1022
      110 TTTCATATTTTCTTACGCTGATCTGAAGCATATATCATTCACAA 67
  
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RESULT 14
US-08-544-332-41/c
; Sequence 41, Application US/08544332
; Patent No. 5935777
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5935777/e1 Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gerard H. Benzen
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/544,332
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,867
FILING DATE: 07-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,755
FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Benzen, Gerard H.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: DE114.C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
FAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 1689 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-544-332-41
  
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Query Match 3.2%; Score 66; DB 2; Length 1689;
Best Local Similarity 43.8%; Pred. No. 0.00072;
Matches 387; Conservative 0; Mismatches 490; Indels 7; Gaps 2;
  
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      139 TGTATATATATATGATTAATTTGATTCATTTATATATGTAAGAAAGATATGTA 198
      943 TATTTTAAAAAATTTAAATTTAGCAAAATTTGCAAAATTAATTAATATATATGTC 884
      199 TGAATTTGATTCATTAATGACATGATGAAAGATTAAGATTTAGTTCTTTTAA 258
      883 CGCTACTCGATTAATTAATATATATATATATATATATATATATATATATATAG 824
      259 AATTCATATATATTTTGGCCAAATTTTGCAAAATATTCATGTTGCAAAATTAAT 318
      823 AATGTTATGATATTAAGAGAAATATATATATATATATATATATATATATATTA 764
      319 TTGAAAAACAAACATATCAACCTTTTTCGACACACTTTTACAAAATCCATTTC 378
      763 ATTAAAGAAACATTTATGCTATATATATATATATATATATATATATATATAT 704
      379 GAAAAAAATTTACATTAACCTGCGAATCAATTTGTATGAAAAATTTAAATTTCC 438
      703 AACGAAAAACAATTTATAGATGATGCAAAAAATATATTTTATCATATATATAT 644
      439 TTTCACCTATATTTGAACTCAAGTGTAAATTTAGAAAAAGAGAAAAATTAATG 498
      643 TATGTCGATGAGCAATCTAATATATATATATATATATATATATATATATAT 584
      499 ACCATTTCATGCGAAATCAAAATTTGTATGAAAAATTTTAAATTTTAAATAT 558
      583 ATTAGGTGTTTAAACTATGAGACATTAATATCTTCATTTGCTTTTATGATCTTAA 524
      559 TGAATTTCAAAGTGTAAATTTAGAAAAAGAGAAAAATTTAAATGACATTTCAT 618
      523 AATAAAGGAGATTTAGATTAATATATATATATATATATATATATATATATAT 464
  
```


Sat Feb 23 11:04:38 2002

us-09-636-826-1.rni

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 23, 2002, 05:14:42 ; Search time 1188.47 Seconds

(without alignments)
18897.134 Million cell updates/sec

Title: US-09-636-826-1

Perfect score: 2090

Sequence: 1 GATATCACACATTCGTCCAT.....TCGGCTTCTGCGTCTGCT

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372869281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: em_estfun:*
2: em_esthum:*
3: em_estlin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hic:*
10: qb_estl:*
11: qb_estl2:*
12: qb_hic:*
13: qb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rtd:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	142	6.8	1885	10	BE420745
2	139.6	6.7	1036	13	CNS031MJ
3	139.4	6.7	879	13	CNS031JRG
4	136.8	6.5	1135	13	CNS031JRG
5	131	6.3	1139	13	AQ897537
6	129.6	6.2	1101	13	CNS000SX
7	129.6	6.2	1201	13	CNS0167M
8	129	6.2	819	11	BS369277
9	129	6.2	1036	13	CNS00599
10	128.6	6.2	982	13	AQ32557V
11	128.2	6.1	1101	13	CNS005V
12	128	6.1	990	13	CNS00601

C 13	127.8	6.1	1059	13	CNS0022B	AL097133 Drosophila
C 14	127.8	6.1	1337	5	BF630719	BF630719 HVSME001
C 15	126.2	6.0	834	10	BI2387	BI2387 F21E20-SP6
C 16	125.4	6.0	757	10	AL514421	AL514421 AL514421
C 17	125.2	6.0	656	13	CNS012JA	AL174415 Tetraodon
C 18	125	6.0	614	13	CNS0152H	AL104045 Drosophila
C 19	125	6.0	1134	11	BF64906	BF64906 HV_CEA001
C 20	124.6	6.0	870	13	AQ30286	AQ30286 nbxb00465
C 21	124.2	5.9	1434	11	BS309133	BS309133 HVSME000
C 22	124	5.9	1101	13	CNS012JN	AL101645 Drosophila
C 23	122.6	5.9	945	13	CNS04DOK	AL285149 Tetraodon
C 24	122.4	5.8	1198	13	B08337	B08337 T19F9-SP6.1
C 25	122.2	5.8	1101	13	CNS0153V	AL104965 Drosophila
C 26	121.8	5.8	859	13	A527955	A527955 ENTCM56TR
C 27	120.8	5.8	1223	13	BI2981	BI2981 T24D11-SP6
C 28	120.6	5.8	850	13	A2186328	A2186328 SP_1006_B
C 29	119.4	5.7	888	13	CNS027EX	AL184578 Tetraodon
C 30	119.2	5.7	619	10	AL514935	AL514935 AL514935
C 31	119.2	5.7	907	13	CNS021JA	AL176953 Tetraodon
C 32	119	5.7	1079	13	CNS0351X	AL228786 Tetraodon
C 33	118.6	5.7	1042	13	CNS0148K	AL103838 Drosophila
C 34	118.4	5.7	974	13	CNS001IT	AL075432 Drosophila
C 35	117.4	5.6	1380	11	BS653591	BS653591 602582321
C 36	117.2	5.6	1185	11	BF273407	BF273407 GA_EB001
C 37	117	5.6	622	13	CNS04ROH	AL304226 Tetraodon
C 38	117	5.6	937	13	CNS0066L	AL062959 Drosophila
C 39	116.8	5.6	781	13	CNS009ND	AL053444 Drosophila
C 40	116.8	5.6	864	13	CNS04NBY	AL298514 Tetraodon
C 41	116.8	5.6	930	11	BS67946	BS67946 HVSME1001
C 42	116.4	5.6	901	11	BF264987	BF264987 HV_CFA001
C 43	116	5.6	576	13	CNS0256N	AL181688 Tetraodon
C 44	115.4	5.5	782	13	CNS06RMZ	AL412161 T7 end of
C 45	115.4	5.5	875	13	A2184435	A2184435 SP_1003_A

ALIGNMENTS

RESULT 1
LOCUS BE420745 1885 bp mRNA EST 24-JUL-2000
DEFINITION HMM002.B02 ITEC HMM Barley Leaf Library Hordeum vulgare cDNA clone
ACCESSION BE420745
VERSION BE420745.1 GI:9418588
KEYWORDS EST
SOURCE EST
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
1 (bases 1 to 1885)

REFERENCE

Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier
S., Dubcovsky, D., Feuillet, C., Gale, M., Graner, A., Gustafson, P.,
Herrmann, R.G., Holton, T., Jacquemont, J.M., Jia, J., Jondreville, P.,
Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y.,
Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M.,
Sorrells, M., Warburton, M., and Wenzel, G.
International Triticeae EST Cooperative (ITEC): Production of
Expressed Sequence Tags for Species of the Triticeae
Unpublished (2000)

JOURNAL

COMMENT Botanisches Institut der LMU
Menzinger Str. 67, D-80638 München GERMANY
Fax: 49 30 171683
Email: hermann@botanik.biologie.uni-muenchen.de
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers

FEATURES

1..1885
/organism="Hordeum vulgare"
/cultivar="Barke"
/db_xref="taxon:4513"

D	b		249	AAA	308
Q	y		370	CCATTTCGAGAAAAAAAAATTTACGTTCACCTGGCAAAATCAAATTGTGTATAAAAATTT	429
D	b		309	AAA	368
Q	y		430	AAATTTTCCCTTCACCCTTAATGTGAACCTCAAGTGTTAAATTTAGAAAAAGGAAAAA	489
D	b		369	AAA	428
Q	y		490	TAAAAAAATGACCATTTCATCGCAAAATCAAATTGTGTAGAAAAAATTAAATTTTATTTT	549
D	b		429	AAA	488
Q	y		550	AAATTAATTTGAAATTCAGAGTGTAAATTTAGAAAAAGGAAAAAATTAATGACCAT	609
D	b		489	AAA	548
Q	y		610	TTCAATTCAAATCAGATTGTGTAGAAAAATTTAAATTTTATTTCAATTAATTTGAAA	669
D	b		549	AAA	608
Q	y		670	CTCAATGCTGACCTTAGAAAAAGGAGAAAAATTAATCATGAATTTTGTAACAAT	729
D	b		609	AAA	668
Q	y		730	CAATTTGTGAATCAGAATTTAGAGTTAGACAAGAAAAAATACTGAATGCTGTATAC	789
D	b		669	AAA	728
Q	y		790	TTTTGCTTACAATTTTGGCATCATTAAGAAATTAATCTCATATCAAAAATCTATTA	849
D	b		729	AAA	788
Q	y		850	TAAATTTACAAAATGAATTAATCCCAAAAAAGAAACATGACGATATTTCGTAAAGAAC	909
D	b		789	AAA	848
Q	y		910	ATCATACTGATTTATTAAGAACATGCCGATTTTGAATTTGGAACAAAAAACTATTGAA	969
D	b		849	AAA	908
Q	y		970	AATCACAAAAATGATATAACAACATACAGACATGAAAGATCTTATTCACAAAAATGGA	1029
D	b		909	AAA	968
Q	y		1030	GGTGACTTAATCTAACTAA 1047	
D	b		969	AAAAAAAAAAAAAAAAAAAAAAAA 986	

RESULT	3
CNSOLJRG/c	
LOCUS	CNSOLJRG 879 bp DNA
DEFINITION	Anopheles gambiae GSS r7 end of clone 14D07 of NotreDame1 library from strain PST of Anopheles gambiae (African malaria mosquito), genomic survey sequence.
ACCESSION	AL147405
VERSION	AL147405.1 GI:7005551
KEYWORDS	GSS.
SOURCE	African malaria mosquito.
ORGANISM	Anopheles gambiae Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles. 1 (bases 1 to 879)
REFERENCE	Genoscope.
AUTHORS	Direct Submission
TITLE	Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
JOURNAL	- Web : www.genoscope.cns.fr) 2 (bases 1 to 879)
REFERENCE	Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
AUTHORS	

JOURNAL	Direct Submission			
TITLE	Submitted (16-FEB-2000) BMR, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France			
COMMENT	This clone is from an <i>A. gambiae</i> BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur.			
FEATURES	Location/Qualifiers			
Source	1. 879			
	/organism="Anopheles gambiae"			
	/strain="PEST"			
	/db_xref="taxon:7165"			
	/clone="14D07"			
	/clone_lib="Notredame1"			
	/note="end : T7"			
BASE COUNT	66 a	38 c	1 g	670 t
ORIGIN	104 others			
Query Match	6.7%	Score 139.4	DB 13	Length 879
Best Local Similarity	43.9%	Pred. No. 4,56-08		
Matches	360	Conservative	47	Mismatches 404
			Indels	9
			Gaps	1

[illegible]

Db	153	AAAAATATAAAAAAAAAAAAAAAAAAATAAAAAAAAAAAVATANAAAAAAAAAAAAAAAANNNNNNNNN	94
OY	1054	TTTTTCAGTTTATTACTACTAGTAATTAGCCCTAAAATA	1093
Db	93	NAAANNCA MBTMTTANNAANNAANNNTATNAAAAAAAAA	54
RESULT	4		
CNS033GO			
LOCUS			
DEFINITION	CNS033GO	1135 bp DNA GSS	15-MAY-2000
	Tetradon nigroviridis genome survey sequence PUC-Ort end of clone		
	208P24 of library G from Tetradon nigroviridis, genomic survey		
	sequence.		
ACCESSION	AL226115		
VERSION	AL226115.1	GI:7885026	
KEYWORDS	GSS; genome survey sequence.		
SOURCE	Tetradon nigroviridis.		
ORGANISM	Tetradon nigroviridis		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;		
	Tetraodontidae; Tetraodon.		
REFERENCE	1 (bases 1 to 1135)		
AUTHORS	Roeßl-Crollius,H., Jallion,O., Dasilva,C., Fizeses,C., Fisher,C.,		
	Bonneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and		
	Weissenbach,J.		
TITLE	Characterization and repeat analysis of the compact genome of the		
JOURNAL	freshwater pufferfish Tetradon nigroviridis		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 1135)		
	Roeßl-Crollius,H., Jallion,O., Dasilva,C., Bonneau,L., Fisher,C.,		
	Bernot,A., Fizeses,C., Wincker,P., Brodter,P., Quetier,F.,		
	Saurin,W. and Weissenbach,J.		
TITLE	Human gene number estimate provided by genome wide analysis using		
JOURNAL	Tetradon nigroviridis DNA sequence		
REFERENCE	Unpublished		
AUTHORS	3 (bases 1 to 1135)		
	Genoscope.		
	Direct Submission		
	Submitted (12-Apr-2000) to the EMBL/GenBank/DBJ databases		
JOURNAL	This sequence is a single read and was generated as part of a large		
COMMENT	scale clone-and sequencing project of the Tetradon nigroviridis		
	genome. For more information, please take a look at		
	http://www.genoscope.cns.fr/Tetradon .		
FEATRES	Location/Qualifiers		
Source	1..1135		
	/organism="Tetradon nigroviridis"		
	/db_xref="taxon:99883"		
	/clone="208P24"		
	/clone_lib="G"		
	/note="genoscope sequence ID : CGAG208DH12SP1-end :		
	PUC-Ort"		
BASE COUNT	863 a 65 c 43 g 124 t 40 others		
ORIGIN			
Query Match	6.5%; Score 136.8; DB 13; Length 1135;		
Best Local Similarity	47.6%; Pred. No. 8e-08;		
Matches 351; Conservative 14; Mismatches 373; Indels 0; Gaps 0;			
OY	310	AAATATAATTTGAACAACAACAATATCAACCTTTTGCGACACACTTTTACAAAAAT	369
Db	248	AA	307
OY	370	CAATTTCGAGAAAAAAAAATTTACATTACTTCGCCAAATCAAATGTGTATGAAAAATT	429
Db	308	AA	367
OY	430	AAATTTTCCTTCACCTATATTTGAACCTCAAGTGTATAAAATTTAGAAAAAGAGAAAA	489
Db	368	AA	427
OY	490	TAAAAAATGCACCTTCATGCGAAATCAAAATGTGTATGAAAAAACCTTAATTTATT	549

[illegible]


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OY      381  AAAAAAAAAATTACATTAATCTGGCAATCAAAATGTGTATCAAAAATTTTAAATTTCCCT 440
        ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      1195  WAAATTAATAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 1136
        ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY      441  TCACCTTAATTTGAACCTCAAAGCTTTAAATTTGAAAAGGAGAAAAATTAATAATGAC 500
        ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rw1ng@clemson.edu
Seq primer: ATTAAACCTCAGTAAAGG
High quality sequence stop: 787.
Location/Qualifiers
1. 819
/organism="Hordeneum vulgare"
/cultivar="Morrex"


```

/db_xref="taxon:4513"
/clone="HVSME10023121f"
/clone.lib="Hordum vulgare 20 DAP spike EST library
HVCN0010 (20 DAP)"
/tissue_type="20 DAP spike"
/lab_host="SOLR"
/notes="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/10
order a clone see http://www.genome.clemson.edu/orders"

```

```

BASE COUNT      12 a      47 c      26 g      734 t
ORIGIN

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```

Query Match      6.2% Score 129; DB 11; Length 819;
Best Local Similarity 48.4%; Pred. No. 8e-07;
Matches 357; Conservative 0; Mismatches 380; Indels 0; Gaps 0;

```

```

QY 311 AATAAATTTTGAACAAACATATCAACCTTTTGGACACACTTTTACAAATC 370
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 812 AAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 753
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 371 CATTTTCAGAAAAAATTTACATTACCTTGCAGAAATCAATTTGTATGAAAAATTTA 430
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 752 AAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 693
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 431 AATTCCTTCCCTTAATTTGAACCTCAAGCTTAATTTAGAAAAAGAGAAAAAT 490
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 692 AAGAGTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 633
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 491 AAAAAATGACATTTTCATGCGAAATCAATTTGTATGAAAAAATTTTATTTTA 550
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 632 AGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 573
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 551 AATTAATTTGAATTCAGAGTTTAAATTTAGAAAAAGAGAAAAATTTAAATGACATT 610
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 572 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 513
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 611 TCATTCAAAAATGATTTGTATGAAAAATTTTAAATTTTATTTCAATTAATTTGAAC 670
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 512 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 453
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 671 TCAAGTGTACATTTTAGAAAAAGAGAAAAATTTAAATGATGAAAAATTTGTAACATC 720
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 452 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 393
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 731 AATTTGCAATTCAGATTTTAGAGTTAGACAGAAAAAAGCTGAATTTGTTTACT 790
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 392 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 333
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 791 TTTCGTTCAATTTTGGATTCATTAAGAAATTTACTGAATTCATTAACCTATTAT 850
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 332 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 273
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 851 AATTTCAAAAAATGATTAACCAAAAAAGAGAAATGATGATTTTCTGTAAGAGACA 910
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 272 AGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 213
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 911 TCATTCAGATTTAAGAAAGATGCGCATTTGTAATTTGAGAAACAAATCTATTCAAA 970
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 212 AAAAAAAGAAAAAAGAAAAAAGAGAGGGGAAAAAAGAAAAAAGAAAAAAGAAAAA 153
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 971 ATCACAAAAAATGATTAACAACATCAAGAAATGAAAGATTTTTCACAAATGAGAG 1030
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 152 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 93
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1031 GTGACCTTAATCTCTAA 1047
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 92 AAAAAAAGAAAAAAGAAAAA 76
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 9
CNS00599/c

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LOCUS      CNS00599      1036 bp      DNA
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BAC11116 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION  AL057797
VERSION    AL057797.1 GI:4932579
KEYWORDS   GSS.
SOURCE     fruit fly.
ORGANISM   Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
            1 (bases 1 to 1036)
REFERENCE  Genoscope.
            Direct Submision
            Submitted (02-JUN-1999) Genoscope - Centre National de Sequence ;
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
            - Web : www.genoscope.cns.fr)
AUTHORS    Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitfly.org/The BDGP Drosophila
            melanogaster BAC library was prepared by Kazuhiro Osoegawa and
            Aaron Mammeter in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
            pl and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES   location/Qualifiers
            source
            1..1036
            /organism="Drosophila melanogaster"
            /db_xref="taxon:7227"
            /clone.lib="RPCI-98"
            /clone="BAC11116"
            /note="end : TET3"
BASE COUNT      64 a      56 c      41 g      701 t      174 others
ORIGIN

```

```

Query Match      6.2% Score 129; DB 13; Length 1036;
Best Local Similarity 42.4%; Pred. No. 7e-07;
Matches 334; Conservative 62; Mismatches 389; Indels 2; Gaps 1;
QY 257 AAAAAATTCATTAATTTTCCCAAAACCTTTGCAAAATATTCATGCGAAATTA 316
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 785 AAGCAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 726
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 317 TTTGAAAAAACAACATATCAACCTTTTGGCAACACTTTTACAAATCATTTT 376
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 725 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 666
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 377 CAGAAAAAATTTTACATTAATTTGCAAAATGATGTAAGAAAAATTTAAATTT 436
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 665 MAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 606
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 437 CTTTCACCTTAATTTGAACCTCAAGCTTTAATTTAGAAAAAGAGAAAAATTA 496
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 605 AAAAAAATTCGAAAGAGAA--AAAAGCTAATTAATTAATTAATTAATTAATTAATTA 548
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 497 TGACATTTTCATGCAAAATTTGTATGAAAAAATTTTAAATTTTAAATATA 556
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 547 STRAATTTTAAKAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 488
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 557 ATTGAATTCAAAGCTTAATTAATTTAGAAAAAGAGAAAAATTTAAATGACATTTTC 616
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 487 AKAKATATKTTTBAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 428
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 617 AAAAAATGATTTGATGAAAAAATTTTAAATTTTATTTCAAAATTAATTTGAACCTCAAG 676
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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[illegible]

RESULT 10
 LOCUS AO325799/c
 DEFINITION AO325799 982 bp DNA GSS 08-JAN-1999
 ACCESSION nbxb0021B14r CUG1 Rice BAC Library Oryza sativa genomic clone
 VERSION AO325799
 KEYWORDS AO325799.1 GI:4117649
 GSS.
 Oryza sativa.
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzae; Oryza.
 1 (bases 1 to 982)
 Wing, R.A. and Dean, R.A.
 A BAC End Sequencing Framework to Sequence the Rice Genome
 Unpublished (1998)
 COMMENT
 CONTACT: Wing RA
 CLEMSON UNIVERSITY GENOMICS INSTITUTE
 CLEMSON UNIVERSITY
 100 JORDAN HALL, CLEMSON, SC 29634, USA
 TEL: 864 656 7288
 FAX: 864 656 4293
 EMAIL: rtwing@clermson.edu
 SEQ PRIMER: GGAAACGCTATGACCATG
 CLASS: BAC ends
 HIGH QUALITY SEQUENCE START: 4
 HIGH QUALITY SEQUENCE STOP: 123.
 FEATURES
 SOURCE 1..982 Location/Qualifiers

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/organism="Oryza sativa"
/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/clone="nxb0021h14r"
/clone_lib="CUGI Rice BAC Library"
/tissue_type="leaf"
/lab_host="E. coli DH10b"
/notes="Vector: pBelogAC11; Site1: HindIII; Site2:
HindIII; Rice is one of the most popular grains in the
world. Half of the world population especially those

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inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of *Arabidopsis*, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from *Oryza sativa*, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), representing the whole library for colony screening."

	Query Match	Similarity	6.2%	Score	128.6	DB	13	Length	982
	Best Local	Similarity	45.8%	Pred	No	8	1e-07		
	Matches	377	Conservative	0	Mismatches	441	Indels	5	Gaps
QY	226	TGAAAAAGTTAACGATTTAGTCTCTTTTAAAAATTCACATATAAATTTTGCCCAAAA							285
DB	974	TGTGAAAGGTAGAGTGAAGATATGATATGATGTTTAAAAATATATATGTAATTAATA							915
QY	286	CTTTTGCAAAATVTCATGTTGCGGAATTAATTTTGAAAAACAAACACATATCAAACTT							345
DB	914	AGATATGAAAGTATGGAATATATAGAAAAGAAATTTTAAATATATATTAATTTTA							860
QY	346	TTTCGACACACTTTTACAAAAATCCATTTTCAGAAAAAAAATTTACATTAACTTGCGA							405
DB	859	ATTATATTATTAATATATGATATATATATATATATATATATATATATATATATAT							800
QY	406	AATCAAAATGTGTAGTAAAAATTTAAATVTCCTTCACCTATATATTGAACCTCAAGTG							465
DB	799	AATTAATTTATATATATATATATATATGATATATATATATATATATATATATAT							740
QY	466	TTAAATTTGAAAAGGAGAAAATTTAAATATGACCATTTCATGCGAAATCAATTTGTG							525
DB	739	AT							600
QY	526	ATGCAAAACCTTAATATTTTAAATTTAAATTTGAATTTCAAGTGTAAATTTTAGAA							585
DB	679	AAAAAAAANNNAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAA							620
QY	586	AAGCAGAAAATTTAAATGACCTTTTCATTCAGAAATCGAGATTGTGTATGAAAAATTTAA							645
DB	619	AAAAAAAANNNAAAAAANAAAAAANAAAAAANAAAAAANNNNNAAAAAANAAAAA							560
QY	646	TTTTTATTTCAAAATATATATGAACTCAAGTGAACATTGTAGAAAAGAGAAAAATTA							705
DB	559	AAAAAAAANNNAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAA							500
QY	706	AAATGATGAAATTTGTAAAAACATCAATTTGTGAAATCAGAAATTTAGAAATTTAGACAGG							765
DB	499	AAAAAAAANNNAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAA							440
QY	766	AAAAAAAACCTGCAATTTGCTTATATCTTTGGTTTACAAATTTTGGGATCTAATGAATATAC							825
DB	439	AAAAAAAANNNAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAA							380
QY	826	TGAATCCATATCAAAAACATATATTAATTTACAAAAATGAATTAACCAAAAAGAGAGA							885
DB	379	AAAAAAAANNNAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAA							320
QY	886	ACATGACGATATTTCTGTAAAGAACATCACTAGTATTAATAAGAACATCGGCATATTTGA							945
DB	319	AAAAAAAANNNAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAA							260
QY	946	ATTGGAACCAAAAAAATCTATTCAAAATTCACAAAAATTGGATTAACAACATCAAGACATG							1005

[illegible]

